

From: Chan, Christina
Sent: Thursday, January 27, 2005 3:14 PM
To: Swope, Sheridan; STIC-Biotech/ChemLib
Subject: RE: 09/771,161

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Swope, Sheridan
Sent: Thursday, January 27, 2005 3:05 PM
To: Chan, Christina
Subject: 09/771,161

Chris, May I have this rushed?

For 09/771,161, pls INTERFERENCE search:

SID 2 against the NT and AA data bases.

SID 93 against the NT and AA data bases.

Sheridan Swope, Ph.D.
Patent Examiner, AU 1652
Recombinant Enzymes
571-272-0943 (voice)
E02B71 Remsen Bld (Office)
E02C70 Remsen Bld (Mailbox)

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Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: 1/28/05
Date Completed: 2/7/05
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search: 1+1- Reverse to
NA Sequence: # 1+1- Reverse to
AA Sequence: # 1+1- Reverse to
Structure: # NA
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: 24/02
WWW/Internet: _____
Other(Specify): _____

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OM nucleic - protein search, using frame_plus_n2p model

Run on: January 28, 2005, 11:42:11 ; Search time 48 Seconds
(without alignments)

4611.864 Million cell updates/sec

Title: US-09-771-161A-2

Perfect score: 2880

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 956278

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1182	41.0	478	US-09-069-023-4	Sequence 4, Appli
3	1182	41.0	530	US-09-069-023-3	Sequence 3, Appli
4	1182	41.0	531	US-09-069-023-1	Sequence 1, Appli
5	1182	41.0	540	US-09-069-023-27	Sequence 27, Appli
6	1182	41.0	540	US-09-345-473E-28	Sequence 28, Appli
7	1176	40.8	540	US-09-019-942-1	Sequence 1, Appli
8	1176	40.8	540	US-09-099-041A-2	Sequence 2, Appli
9	1176	40.8	540	US-09-245-281-2	Sequence 1, Appli
10	1176	40.8	540	US-09-470-271-1	Sequence 2, Appli
11	1176	40.8	540	US-09-207-359B-2	Sequence 2, Appli
12	1176	40.8	540	US-09-340-620A-2	Sequence 2, Appli

13	1176	40.8	540	4	US-09-865-364-2	Sequence 2, Appli
14	1176	40.8	540	4	US-09-748-537-1	Sequence 1, Appli
15	867	30.1	167	3	US-09-069-023-6	Sequence 6, Appli
16	632	21.9	131	3	US-09-099-041A-5	Sequence 5, Appli
17	632	21.9	131	3	US-09-245-281-5	Sequence 5, Appli
18	632	21.9	131	3	US-09-207-359B-5	Sequence 5, Appli
19	632	21.9	131	4	US-09-340-620A-5	Sequence 5, Appli
20	632	21.9	131	4	US-09-865-364-5	Sequence 5, Appli
21	548	19.0	110	4	US-09-207-359B-6	Sequence 6, Appli
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26	451	15.7	90	4	US-09-841-879B-10	Sequence 10, Appl
27	149.5	5.2	109	4	US-09-340-620A-71	Sequence 71, Appl
28	143.5	5.0	95	4	US-09-841-879B-12	Sequence 12, Appl
29	122.5	4.3	164	3	US-09-245-281-41	Sequence 41, Appl
30	122.5	4.3	164	4	US-09-207-359B-41	Sequence 41, Appl
31	122.5	4.3	164	4	US-09-340-620A-41	Sequence 41, Appl
32	122.5	4.3	164	4	US-09-865-364-41	Sequence 41, Appl
33	122.5	4.3	249	3	US-09-245-281-39	Sequence 39, Appl
34	122.5	4.3	249	4	US-09-207-359B-39	Sequence 39, Appl
35	122.5	4.3	249	4	US-09-340-620A-39	Sequence 39, Appl
36	122.5	4.3	249	4	US-09-865-364-39	Sequence 39, Appl
37	122.5	4.3	409	4	US-09-207-359B-46	Sequence 46, Appl
38	122.5	4.3	409	4	US-09-865-364-46	Sequence 46, Appl
39	122.5	4.3	953	3	US-09-099-041A-8	Sequence 8, Appli
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41	122.5	4.3	953	4	US-09-207-359B-8	Sequence 8, Appli
42	122.5	4.3	953	4	US-09-340-620A-8	Sequence 8, Appli
43	122.5	4.3	953	4	US-09-865-364-8	Sequence 8, Appli
44	119	4.1	100	3	US-09-099-041A-10	Sequence 10, Appl
45	119	4.1	100	3	US-09-245-281-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-069-023-5
; Sequence 5: Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-5

Alignment Scores:
Pred. No.: 7.91e-132 Length: 284
Score: 1182.00 Matches: 227
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.56% Mismatches: 0
Query Match: 41.04% Indels: 0
DB: 3 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-069-023-5 (1-284)

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Db 57 LysLeuGlnSerValSerAlaIleHisLeuCyAspLysLysMetGluLeuSer 76

QY 392 CTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 451

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Db      77  LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 96
      452  GAAATAGTGGTCTCTCTGAACTTCAAGTCCCTCCAGCTCCTCAAGACAAATGATTTT 511
      97  GluAsnSerGlySerProGlnThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 116
      512  TTATCTAGAAAGCTCAAGACTGTTTATTTATGAAGCTGCATCAGTCTCTGGAATCAC 571
      117  LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 136
      572  AGTTGGATAGCACCATTCTTGATCTCAAGGCTGCAATTCGTATCATCAAGACCACT 631
      137  SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 156
      632  CCATGCTCTTACCAATAATAATCACTCTCAAGTGCAGGAACTCAGAACGCTCTGCAG 691
      157  ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 176
      692  CTGGTATAGCCAGCAGTGGATCCAGACCAAGGGAAGACATTTGTGAACCAATGACA 751
      177  ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 196
      752  GAAGCTGCTTAAACAGTCGTAGATGCCCTTCTGTCAGGAGCTTGATCATGAAGAG 811
      197  GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 216
      812  GACTATGAAGTGTAGTACCAAGCTCAGACGCTCAAGAGCTCAAGAACTCAGAACTACTAGAC 871
      217  AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 236
      872  ACTACTGACATCAAGGAGGAATTTGCCAAGTTATAGTACAAAATTTGAAGTAAAC 931
      237  ThrThrAspIleGlnGluPheAlaLysValIleValGlnLysLeuLysAspAsn 256
      932  AAACAAATGGCTTTCAGCCTTACCCGGAATACTTGTGGTTTCTAGATCACCATCTTTA 991
      257  LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 276
      992  AATTACTTCAAAATAAAAGCATG 1015
      277  AsnLeuLeuGlnAsnLysSerMet 284

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RESULT 2

US-09-069-023-4
; Sequence 4, Application US/09069023A
; Patent No. 6348573

GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel

; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS

; FILE REFERENCE: UM-0333

; CURRENT APPLICATION NUMBER: US/09/069,023A

; CURRENT FILING DATE: 1998-04-27

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 478

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-069-023-4

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Query Match:	41.04%	Indels:	0
DB:	3	Gaps:	0

US-09-771-161A-2 (1-1669) x US-09-069-023-4 (1-478)

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QY      392  CTGACATACCTGTTAAATCATGGTCCACAAGGGAATCATGTGGATCCTCTCAGCTCCAT 451
Db      271  LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 290
QY      452  GAAATAGTGGTCTCTCTGAAACTTCAAGTCCCTCCAGCTCCTCAAGACAAATGATTTT 511
Db      291  GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 310
QY      512  TTATCTAGAAAGCTCAAGACTGTTTATTTATGAAGCTGCATCAGTCTCTGGAATCAC 571
Db      311  LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 330
QY      572  AGTTGGATAGCACCATTCTTGATCTCAAGGCTGCAATTCGTATCATCAAGACCACT 631
Db      331  SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 350
QY      632  CCATGCTCTTACCAATAATAATCACTCTCAAGTGCAGGAACTCAGAACGCTCTGCAG 691
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QY      692  CTGTATAGCCAGCAGTGGATCCAGACGAAAGGGAAGACATTTGTGAACCAATGACA 751
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QY      752  GAAGCTGCTTAAACAGTCGTAGATGCCCTTCTGTCAGGAGCTTGATCATGAAGAG 811
Db      391  GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 410
QY      812  GACTATGAAGTGTAGTACCAAGCTCAGACGCTCAAGGAGCTCAAGAACTCAGAACTACTAGAC 871
Db      411  AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 430
QY      872  ACTACTGACATCAAGGAGGAATTTGCCAAGTTATAGTACAAAATTTGAAGTAAAC 931
Db      431  ThrThrAspIleGlnGluPheAlaLysValIleValGlnLysLeuLysAspAsn 450
QY      932  AAACAAATGGCTTTCAGCCTTACCCGGAATACTTGTGGTTTCTAGATCACCATCTTTA 991
Db      451  LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 470
QY      992  AATTACTTCAAAATAAAAGCATG 1015
Db      471  AsnLeuLeuGlnAsnLysSerMet 478

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RESULT 3

US-09-069-023-3

; Sequence 3, Application US/09069023A

; Patent No. 6348573

GENERAL INFORMATION:

; APPLICANT: Nunez, Gabriel

; APPLICANT: Inohara, Naohiro

; APPLICANT: Koseki, Takeyoshi

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS

; FILE REFERENCE: UM-0333

; CURRENT APPLICATION NUMBER: US/09/069,023A

; CURRENT FILING DATE: 1998-04-27

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 530

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-069-023-3

Alignment Scores:

Pred. No.:	1-09e-131	Length:	530
Score:	1182.00	Matches:	227

Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.56% Mismatches: 0
Query Match: 41.04% Indels: 0
DB: 3 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-069-023-3 (1-530)

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QY 392 CTGAACATACCTGTAATCATGTCCACAAGAGGAATCATGTGCATCTCAGTCCAT 451
Db 323 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 342

QY 452 GAAATAGTGGTTCCTCAAGTGCCTCAAGTGCCTCCTCAAGACATGATGTTT 511
Db 343 GluAsnSerGlySerProGlnThrSerArgSerLeuProAlaProGlnAspAsnApphe 362

QY 512 TTATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCAGTCTGCGAAATCAC 571
Db 363 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 382

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QY 632 CCATGCTCTTCACCAATAAATCCACTCTCAACTGCAGGAACTCAGAACTCTGCAG 691
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QY 692 CTGTGTATAGCCAGAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACA 751
Db 423 ProGlyIleAlaGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 442

QY 752 GAAGCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCAGGACTTGATCATGAAGAG 811
Db 443 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 462

QY 812 GACTATGACTTCTAGTACCAAGCTTACAGGACCTCAAGGACCTCAAAAGTACAGAAATGACA 871
Db 463 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 482

QY 872 ACTACTGCATCCAAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATAAC 931
Db 483 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 502

QY 932 AAACAAATGGTCTTCAGCCTTACCGGAAATACCTTGTTGTTCTAGATCACCATCTTTA 991
Db 503 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 522

QY 992 AATTTACTTCAAAATAAAGCATG 1015
Db 523 AsnLeuLeuGlnAsnLysSerMet 530
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RESULT 4

US-09-069-023-1
; Sequence 1, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Koseki, Takeyoshi
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; FILE REFERENCE: UM-03333
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 531
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-069-023-1

Alignment Scores:
Pred. No.: 1,09e-131 Length: 531
Score: 1182.00 Matches: 227
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.56% Mismatches: 0
Query Match: 41.04% Indels: 0
DB: 3 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-069-023-1 (1-531)

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QY 392 CTGAACATACCTGTAATCATGTCCACAAGAGGAATCATGTGCATCTCAGTCCAT 451
Db 324 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 343

QY 452 GAAATAGTGGTTCCTCAAGTGCCTCAAGTGCCTCCTCAAGACATGATGTTT 511
Db 344 GluAsnSerGlySerProGlnThrSerArgSerLeuProAlaProGlnAspAsnApphe 363

QY 512 TTATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCAGTCTGCGAAATCAC 571
Db 364 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 383

QY 572 AGTTGGATAGCACCAATTCCTGATCTCAAGGGCTGCATTCCTGATCACAAGACCAT 631
Db 384 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 403

QY 632 CCATGCTCTTCACCAATAAATCCACTCTCAACTGCAGGAACTCAGAACTCTGCAG 691
Db 404 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 423

QY 692 CTGTGTATAGCCAGAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACA 751
Db 424 ProGlyIleAlaGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 443

QY 752 GAAGCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCAGGACTTGATCATGAAGAG 811
Db 444 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 463

QY 812 GACTATGACTTCTAGTACCAAGCTTACAGGACCTCAAGGACCTCAAAAGTACAGAAATGACA 871
Db 464 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 483

QY 872 ACTACTGCATCCAAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATAAC 931
Db 484 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 503

QY 932 AAACAAATGGTCTTCAGCCTTACCGGAAATACCTTGTTGTTCTAGATCACCATCTTTA 991
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QY 992 AATTTACTTCAAAATAAAGCATG 1015
Db 524 AsnLeuLeuGlnAsnLysSerMet 531
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RESULT 5

US-09-069-023-27
; Sequence 27, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069, 023A

Patent No. 6033855
 GENERAL INFORMATION:
 APPLICANT: Bertin, John
 TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
 TITLE OF INVENTION: DOMAIN POLYPEPTIDES
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FastSeq for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/019,942
 FILING DATE: 06-FEB-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Meiklejohn, Ph.D., Anita L.
 REGISTRATION NUMBER: 35,283
 REFERENCE/DOCKET NUMBER: 07334/068001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 540 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-019-942-1

Alignment Scores:
 Pred. No.: 5,7e-131 Length: 540
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 Best Local Similarity: 99.12% Mismatches: 1
 Query Match: 40.83% Indels: 0
 DB: 3 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-019-942-1 (1-540)

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 QY 392 CTGAACATACCTGTAAATCATGTCTCCACAGAGGAATCATGTGATCCTCTCAGCTCCAT 451
 Db 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 352
 QY 452 GAAATAGTGGTTCCTGAACTTCAAGTCCCTCCAGCTCCTCAAGACAAATGATTTT 511
 Db 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372
 QY 512 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCAGCTGCTGGAATCAC 571
 Db 373 LeuSerArgLysAlaGlnAspCysThrPheMetLysLeuHisCysProGlyAsnHis 392
 QY 572 AGTTGGATGAGCACCATTCTGGATCTCAAAGGGCTGCATTCTGTGATCACAGACCAT 631
 Db 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaPheCysAspHisLysThrIle 412
 QY 632 CAGTCTCTTCAGCAATAATAATCCACTCTCACTGCGAGAACTCAGAACGTCGCGAG 691
 Db 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432

QY 692 CTTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTCTGAACCAATGACA 751
 Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgLysAlaIleValAsnGlnMetThr 452
 QY 752 GAAGCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAAGAG 811
 Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
 QY 812 GACTATGAACCTTTAGTAGTACCAGCTCAAGGACCTCAAAAGTCAGACAATTACTAGAC 871
 Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
 QY 872 ACTACTGACATCCAGGAGCAAGATTGCAAGATTATAGTACAAAATTTGAAAGATAAC 931
 Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
 QY 932 AAACAAATGGTCTTCAGCCTTACCCGAAATCTTGTGTTTCTAGATCACCATCTTTA 991
 Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532
 QY 992 AATTTACTTCAAAATAAAGCATG 1015
 Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 8

US-09-099-041A-2
 Sequence 2, Application US/09099041A
 Patent No. 6340576
 GENERAL INFORMATION:
 APPLICANT: Bertin, John
 TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
 TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
 FILE REFERENCE: 07334-076001
 CURRENT APPLICATION NUMBER: US/09/099,041A
 CURRENT FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 09/019,942
 PRIOR FILING DATE: 1998-02-06
 NUMBER OF SEQ ID NOS: 37
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 540
 TYPE: PRP
 ORGANISM: Homo sapiens
 US-09-099-041A-2

Alignment Scores:
 Pred. No.: 5,7e-131 Length: 540
 Score: 1176.00 Matches: 226
 Percent Similarity: 99.56% Conservative: 1
 Best Local Similarity: 99.12% Mismatches: 1
 Query Match: 40.83% Indels: 0
 DB: 3 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-099-041A-2 (1-540)

QY 332 CAGTTACAGAGTGTTCAGAGTGCATTACCTATGTGACAGAGAAATGGAATTATCT 391
 Db 313 LysLeuGlnSerValSerSerAlaIleHisLeuCyAspLysLysMetGluLeuSer 332
 QY 392 CTGAACATACCTGTAAATCATGTCTCCACAGAGGAATCATGTGATCCTCTCAGCTCCAT 451
 Db 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 352
 QY 452 GAAATAGTGGTTCCTGAACTTCAAGTCCCTCCAGCTCCTCAAGACAAATGATTTT 511
 Db 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372
 QY 512 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCAGCTGCTGGAATCAC 571
 Db 373 LeuSerArgLysAlaGlnAspCysThrPheMetLysLeuHisCysProGlyAsnHis 392
 QY 572 AGTTGGATGAGCACCATTCTGGATCTCAAAGGGCTGCATTCTGTGATCACAGACCAT 631

Db 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 412

Qy 632 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGTCGCGAG 691

Db 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432

Qy 692 CTGGTATAGCCAGCAGTGGATGCCAGCAAGAAAGGAGACATTTGTGAACCAAAATGACA 751

Db 433 ProGlyIleAlaGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452

Qy 752 GAAGCTGCTTAACACGTCGTAGATGCCCTTCTGTCAGGACTTCATCATGAAAGAG 811

Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472

Qy 812 GACTATGAATCTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAAATTTACTAGAC 871

Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492

Qy 872 ACTACTGACATCAAGGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATAC 931

Db 493 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512

Qy 932 AAACAATGGCTTCAGCCTTACCGGAAATACTTGTGTTTCTAGATCACCATCTTTA 991

Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532

Qy 992 AATTACTTCAAAATAAAAGCATG 1015

Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 9

US-09-245-281-2

; Sequence 2, Application US/09245281

; Patent No. 6369196

; GENERAL INFORMATION:

; APPLICANT: Bertin, John

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY

; FILE REFERENCE: 07334/118001

; CURRENT APPLICATION NUMBER: US/09/245,281

; CURRENT FILING DATE: 1999-02-05

; EARLIER APPLICATION NUMBER: US 09/207,359

; EARLIER FILING DATE: 1998-12-08

; EARLIER APPLICATION NUMBER: US 09/099,041

; EARLIER FILING DATE: 1998-06-17

; EARLIER APPLICATION NUMBER: US 09/019,942

; EARLIER FILING DATE: 1998-02-06

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 540

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-245-281-2

Alignment Scores:

Pred. No.: 5,7e-131 Length: 540

Score: 1176.00 Matches: 226

Percent Similarity: 99.56% Conservative: 1

Best Local Similarity: 99.12% Mismatches: 1

Query Match: 40.83% Indels: 0

DB: 3 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-245-281-2 (1-540)

Qy 332 CAGTTACAGAGTGTTCAGTGCATTCACCTATGTGACAGAAAGAAATGGAATATCT 391

Db 313 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332

Qy 392 CTGACATCTCTGTAATCATGTCGTCACAGAGCAATCATGTGATCTCTCAGCTCCAT 451

Db 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 352

Qy 452 GAAATAGTGGTCTCTCTGAAACTTCAAGTCCCTGCCAGCTCCTCAAGCAATGATTTT 511

Db 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPhe 372

Qy 512 TTATCTGAAAGAGTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCTCTGGAAATCAC 571

Db 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392

Qy 572 AGTTGGGATGACCACTTTCTGGATCTCAAGGCTGCTATCTGTGTGATCACAAGCACT 631

Db 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 412

Qy 632 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGTCGCGAG 691

Db 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432

Qy 692 CTGGTATAGCCAGCAGTGGATGCCAGCAAGAAAGGAGACATTTGTGAACCAAAATGACA 751

Db 433 ProGlyIleAlaGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452

Qy 752 GAAGCTGCTTAACACGTCGTAGATGCCCTTCTGTCAGGACTTCATCATGAAAGAG 811

Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472

Qy 812 GACTATGAATCTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAAATTTACTAGAC 871

Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492

Qy 872 ACTACTGACATCAAGGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATAC 931

Db 493 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512

Qy 932 AAACAATGGCTTCAGCCTTACCGGAAATACTTGTGTTTCTAGATCACCATCTTTA 991

Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532

Qy 992 AATTACTTCAAAATAAAAGCATG 1015

Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 10

US-09-470-271-1

; Sequence 1, Application US/09470271

; Patent No. 6410689

; GENERAL INFORMATION:

; APPLICANT: Bertin, John

; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT

; TITLE OF INVENTION: DOMAIN POLYPEPTIDES

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: FASTSEQ for Windows Version 2.0b

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/470,271

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/019,942

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Meiklejohn, Ph.D., Anita L.

; REGISTRATION NUMBER: 35,283

; REFERENCE/DOCKET NUMBER: 07334/068001

; TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-470-271-1

Alignment Scores:
Pred. No.: 5,7e-131 Length: 540
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 40.83% Indels: 0
DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-470-271-1 (1-540)

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QY 332 CAGTTACAGAGTGTTCCTGAACTTCAAGTCCCTCCAGTCTCCTCAAGACAAATGGAATATCT 391
DB 313 LysLeuGlnSerValSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332
QY 392 CTGAACATACCTGTAATCATGTCCCAAGAGGAATCATGTGATCCTCTCAGCTCCAT 451
DB 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 352
QY 452 GAAATAGTGGTTCCTGAACTTCAAGTCCCTCCAGTCTCCTCAAGACAAATGATTTT 511
DB 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPhe 372
QY 512 TTATCTAGAAAGCTCAAGACTGTATTTATGAAGTCCATCATCAGTCTCTGGAATCAT 571
DB 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392
QY 572 AGTTGGGATAGACACCATTTCTGATCTCAAGGGCTGCAATCTGTGATCACAAGACCACT 631
DB 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 412
QY 632 CAGTCTTTCAGCAATAATAATCACTCTCAACTGCGAGGAACTCAGAACGCTGCGAG 691
DB 413 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
QY 692 CCTGGTATAGCCAGAGTGGATCCAGACCAAGGGAAGACATTTGTGATCAAGAAATGACA 751
DB 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452
QY 752 GAAGCTGCTTAACCCAGTCGCTAGATGCCCTTCTGTCAGGGACTTGATCATGAAGAG 811
DB 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
QY 812 GACTATGAATCTGTTAGTACCAAGCCTCAAGACCTCAAAAGTTCAGACAAATTTACTAGAC 871
DB 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGACATCCAAAGAGAGATTTGCCAAAGTTATAGTACAAAATTTGAAAGTAAC 931
DB 493 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AAACAAATGGGTCTTCAGCTTACCCGGAATACTTGTGTTTCTAGATCACCATCTTTA 991
DB 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 532
QY 992 AATTACTTCAAAATAAAGCATG 1015
DB 533 AsnLeuLeuGlnAsnLysSerMet 540
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RESULT 11

US-09-207-359B-2
Sequence 2, Application US/09207359B
Patent No. 6469140

GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-112001
CURRENT APPLICATION NUMBER: US/09/207,359B
PRIOR FILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: US/09/099,041
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US/09/019,942
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 540
TYPE: PRT
ORGANISM: Homo sapiens
US-09-207-359B-2

Alignment Scores:

Pred. No.: 5,7e-131 Length: 540
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 40.83% Indels: 0
DB: 4 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-207-359B-2 (1-540)

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QY 332 CAGTTACAGAGTGTTCCTGAACTTCAAGTCCCTCCAGTCTCCTCAAGACAAATGGAATATCT 391
DB 313 LysLeuGlnSerValSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332
QY 392 CTGAACATACCTGTAATCATGTCCCAAGAGGAATCATGTGATCCTCTCAGCTCCAT 451
DB 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 352
QY 452 GAAATAGTGGTTCCTGAACTTCAAGTCCCTCCAGTCTCCTCAAGACAAATGATTTT 511
DB 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPhe 372
QY 512 TTATCTAGAAAGCTCAAGACTGTATTTATGAAGTCCATCATCAGTCTCTGGAATCAT 571
DB 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392
QY 572 AGTTGGGATAGACACCATTTCTGATCTCAAGGGCTGCAATCTGTGATCACAAGACCACT 631
DB 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 412
QY 632 CAGTCTTTCAGCAATAATAATCACTCTCAACTGCGAGGAACTCAGAACGCTGCGAG 691
DB 413 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
QY 692 CCTGGTATAGCCAGAGTGGATCCAGACCAAGGGAAGACATTTGTGATCAAGAAATGACA 751
DB 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452
QY 752 GAAGCTGCTTAACCCAGTCGCTAGATGCCCTTCTGTCAGGGACTTGATCATGAAGAG 811
DB 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
QY 812 GACTATGAATCTGTTAGTACCAAGCCTCAAGACCTCAAAAGTTCAGACAAATTTACTAGAC 871
DB 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGACATCCAAAGAGAGATTTGCCAAAGTTATAGTACAAAATTTGAAAGTAAC 931
DB 493 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AAACAAATGGGTCTTCAGCTTACCCGGAATACTTGTGTTTCTAGATCACCATCTTTA 991
DB 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 532
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QY 992 AATTACTTCAAAATAAAGCATG 1015
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 12
US-09-340-620A-2
; Sequence 2, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340,620A
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-340-620A-2

Alignment Scores:
Pred. No.: 540
Score: 1176.00
Percent Similarity: 99.56%
Best Local Similarity: 99.12%
Query Match: 40.83%
Indels: 0
Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-340-620A-2 (1-540)
QY 332 CAGTTACAGAGTGTTCAGTGCCTTCACTATGTGACAGAGAAATGGAATTTATCT 391
Db 313 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332
QY 392 CTGAACATACCTGTAATCATGTCCACAGAGGAATCATGGATCTCTCAGCTCCAT 451
Db 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 352
QY 452 GAAATAGTGGTCTCTCTGAAACTTCAAGGCTCCCTGAGCTCTCAAGACAAATGATTTT 511
Db 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372
QY 512 TTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCATCTGCTGGAATCAC 571
Db 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392
QY 572 AGTTGGATAGCACCATTTCTGGATCTCAAGGCTCTCAAGGCTCCCTGAGCTCTCAAGACAAATGATTTT 511
Db 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaIlePheCysAspHisLysThrIle 412
QY 632 CCATCTCTTACGAAATATAATCACTCTCACTGAGGAAATCTCAGAACGCTGTCGAG 691
Db 413 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
QY 692 CCGGTATAGCCACAGTGGATTCAGAGAAAGGAGACATTTGTGAAACCAATGACA 751
Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452
QY 752 GAAGCCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCAGGACTTCTCATCATGAAACAG 811
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspLeuIleWetLysGlu 472
QY 812 GACTATGAACCTTGTAGTACCAAGCCTCAAGGACCTCAAAAGTGCAGACAATTACTAGAC 871
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Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGACATCCAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTGAAAGATAAC 931
Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AAACAAATGGGTCTTTCAGCCTTACCCGAAATACTTGTGGTTTCTAGATCACCATCTTTA 991
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532
QY 992 AATTACTTCAAAATAAAGCATG 1015
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 13
US-09-865-364-2
; Sequence 2, Application US/09865364
; Patent No. 6613521
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/865,364
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-865-364-2

Alignment Scores:
Pred. No.: 540
Score: 1176.00
Percent Similarity: 99.56%
Best Local Similarity: 99.12%
Query Match: 40.83%
Indels: 0
Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-865-364-2 (1-540)
QY 332 CAGTTACAGAGTGTTCAGTGCCTTCACTATGTGACAGAGAAATGGAATTTATCT 391
Db 313 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332
QY 392 CTGAACATACCTGTAATCATGTCCACAGAGGAATCATGGATCTCTCAGCTCCAT 451
Db 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 352
QY 452 GAAATAGTGGTCTCTCTGAAACTTCAAGGCTCCCTGAGCTCTCAAGACAAATGATTTT 511
Db 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372
QY 512 TTATCTAGAAAGCTCAAGACTGTTATTTATGAAGCTGCATCATCTGCTGGAATCAC 571
Db 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392
QY 572 AGTTGGATAGCACCATTTCTGGATCTCAAGGCTCTCAAGGCTCCCTGAGCTCTCAAGACAAATGATTTT 511
Db 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaIlePheCysAspHisLysThrIle 412
QY 632 CCATCTCTTACGAAATATAATCACTCTCACTGAGGAAATCTCAGAACGCTGTCGAG 691
Db 413 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
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Qy	692	CCTGGTATACCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACA	751
Db	433	ProGlyIleAlaGlnInTrpIleGlnSerIysArgGluAspIleValAsnGlnMetThr	452
Qy	752	GRAGCCTGCCTTAACCAAGTCGTAGATGCCCTTCTGTCCAGGACCTTGATCATGAAAGAG	811
Db	453	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu	472
Qy	812	GACTATTGAACCTTGTAGTACCAAGCCTCAAGGACCTCAAAGTCACACAAATTACTAGAC	871
Db	473	AspIlyrGluLeuValSerThrIys8ProThrArgThrSerIysValArgGlnLeuLeuAsp	492
Qy	872	ACTACTGCATCCAAAGGAGAGAAATTCGCAAAAGTTATTAGTACAAAAATTGAAAGATAAC	931
Db	493	ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn	512
Qy	932	AAACAAATGGGTCTTCAGCCTTACC CGGAAATACTGTGGTTCTTAGATCACCATCTTTTA	991
Db	513	LysGlnMetGlyLeuGlnProTyrProGluIleValValSerArgSerProSerLeu	532
Qy	992	AATTTACTTCAAAATAAAGCATG	1015
Db	533	AsnLeuLeuGlnAsnLysSerMet	540

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Db      ||||||| 41 CysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 60
QY      ||||||| 695 GGTATAGCCACGAGTGGATCCAGAGCAAAAGGAGACATTGTGAACCAATGACAGAA 754
Db      ||||||| 61 GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThrGlu 80
QY      ||||||| 755 GCTGCTTTAACCCAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAAGAGGAC 814
Db      ||||||| 81 AlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleWetLysGluAsp 100
QY      ||||||| 815 TATGAACCTTGTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATTACTAGACACT 874
Db      ||||||| 101 TyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 120
QY      ||||||| 875 ACTGACATCCAGGAGAGAAGAAATTGCCAAAGTTATAGTACAAAATTGAAAGATACAAA 934
Db      ||||||| 121 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsnLys 140
QY      ||||||| 935 CAAATGGGTCTTCAGCCTTACCCGGAATACTTGTGGTTTCTAGATCACCATCTTTAAAT 994
Db      ||||||| 141 GlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeuAsn 160
QY      ||||||| 995 TTACTTCAAAATAAAGCATG 1015
Db      ||||||| 161 LeuLeuGlnAsnLysSerMet 167
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Search completed: January 28, 2005, 12:37:38
Job time : 66 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2005, 22:16:24 ; Search time 164 Seconds
(without alignments)
7233.577 Million cell updates/sec

Title: US-09-771-161A-2
Perfect score: 1669
Sequence: 1 acctagtattaccagata.....caacagcctgatgtgtgtaaa 1669

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 35539441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
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3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
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5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfilesi.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1308	78.4	2501	4	US-09-920-663-3
2	1308	78.4	2502	3	US-09-069-023-2
3	731.8	43.8	1931	3	US-09-019-942-2
4	731.8	43.8	1931	3	US-09-099-041A-1
5	731.8	43.8	1931	3	US-09-245-281-1
6	731.8	43.8	1931	4	US-09-470-271-2
7	731.8	43.8	1931	4	US-09-207-359B-1
8	731.8	43.8	1931	4	US-09-340-620A-1
9	731.8	43.8	1931	4	US-09-865-364-1
10	731.8	43.8	1931	4	US-09-748-537-2
11	695.4	41.7	1060	3	US-09-023-655-684
12	681.8	40.9	1620	3	US-09-099-041A-3
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15	681.8	40.9	1620	4	US-09-340-620A-3
16	681.8	40.9	1620	4	US-09-865-364-3
17	54.2	3.2	19124	2	US-08-487-826B-13
18	52.8	3.2	20674	4	US-09-641-638-651
19	52.8	3.2	20674	4	US-10-170-097-651
20	51.8	3.1	1141	4	US-09-806-708B-22
21	51.2	3.1	1141	4	US-09-806-708B-22
22	50.4	3.0	832	4	US-09-621-976-2813
23	48	2.9	6152	3	US-08-973-462-1
24	48	2.9	6156	4	US-10-204-708-60
25	47.8	2.9	6583	4	US-10-204-708-25
26	47.6	2.9	396	4	US-09-640-173-53
27	47.6	2.9	396	4	US-09-713-550-53

28	47.6	2.9	396	4	US-09-825-294-53	Sequence 53, Appl
29	47.6	2.9	396	4	US-09-970-966-53	Sequence 53, Appl
30	47.6	2.9	834	3	US-08-998-416-305	Sequence 305, Appl
31	47.6	2.9	10144	4	US-10-204-708-93	Sequence 93, Appl
32	47.4	2.8	1055	4	US-09-806-708B-23	Sequence 23, Appl
33	47.4	2.8	5610	4	US-10-204-708-54	Sequence 54, Appl
34	47.4	2.8	5852	1	US-07-867-106-2	Sequence 2, Appl
35	47.4	2.8	640681	4	US-09-790-988-1	Sequence 1, Appl
36	47	2.8	640681	4	US-09-790-988-1	Sequence 1, Appl
37	46.4	2.8	1055	4	US-09-806-708B-23	Sequence 23, Appl
38	46.2	2.8	474	4	US-09-621-976-18033	Sequence 18033, A
39	46	2.8	5562	4	US-10-204-708-63	Sequence 63, Appl
40	45.8	2.7	701	3	US-08-998-416-701	Sequence 701, Appl
41	45.8	2.7	832	4	US-09-621-976-2813	Sequence 2813, Ap
42	45.8	2.7	6669	4	US-10-204-708-6	Sequence 6, Appl
43	45.8	2.7	8920	2	US-08-446-855A-1	Sequence 1, Appl
44	45.8	2.7	8920	2	US-09-150-741-1	Sequence 1, Appl
45	45.8	2.7	9347	4	US-10-204-708-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-09-920-663-3
; Sequence 3, Application US/09920663
; Patent No. 6426221
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; TITLE OF INVENTION: ANTISENSE MODULATION OF RIP2 EXPRESSION
; FILE REFERENCE: RTS-0233
; CURRENT APPLICATION NUMBER: US/09/920,663
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 3
; LENGTH: 2501
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (225)...(1847)
US-09-920-663-3

Query Match	78.4%	Score 1308;	DB 4;	Length 2501;
Best Local Similarity	99.0%	Pred. No. 4.8e-302;		
Matches 1329;	Conservative 0;	Mismatches 5;	Indels 8;	Gaps 1;
QY	331	ACAGTTACAGAGTGTTC	AAAGTGC	CAATTCACCTATGTGACAGAGAAATGGAATTATC 390
Db	1160	AAAGTTACAGAGTGTTC	AAAGTGC	CAATTCACCTATGTGACAGAGAAATGGAATTATC 1219
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QY	631	TCATGCTCTTCCAGCA	ATTAATTAAT	TCCACTCTCAACTGAGGAACTCAGAACGCTGCA 690
Db	1460	TCATGCTCTTCCAGCA	ATTAATTAAT	TCCACTCTCAACTGAGGAACTCAGAACGCTGCA 1519
QY	691	GCTGTATAGCCAGCA	GTCAGTGGAT	CCAGAGCAAAAGGAAGACATTGTGAACCAATGAC 750

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Qy 811 GGACTATGACTTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCAAGCAATTAATAC 870
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Qy 931 CAAACAAATGGGCTTCCAGCTTACCAGGAAATACCTTGGTGGTTCATGATCAATCTTT 990
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Qy 1051 AAAGGATATTTATATCTCTGTTGCTTGGACTTTTATATAAAATCCGTCAGTATTA 1110
Db 1880 AAAGGATATTTATATCTCTGTTGCTTGGACTTTTATATAAAATCCGTCAGTATTA 1939
Qy 1111 AGCTTTTAAAGGTTCTTGGTAAATATAGTCTCCCTCAAGACATGACATGACATTTT 1170
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Db 2480 ATAAAGTCAACAGCTGATGTG 2501
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RESULT 2

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US-09-069-023-2
; Sequence 2, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
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; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; FILE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-0333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2502
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-069-023-2
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Query Match 78.4%; Score 1308; DB 3; Length 2502;
Best Local Similarity 99.0%; Pred. No. 4.8e-302;
Matches 1329; Conservative 0; Mismatches 5; Indels 8; Gaps 1;
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Qy 331 ACAGTTACAGAGTGTTCAGGTGCCATTCACCTATGTGACAAAGAAATGAATATC 390
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Db CGGCTTCCCTGCTCCCAATTTTAAACCTCAGGCTTCCCTACTGTCAACCAACCAAGCTAA 2480
QY ATAAAGTCAACGCTGATGTG 1664
Db ATAAAGTCAACGCTGATGTG 2502

RESULT 3

US-09-019-942-2

Sequence 2, Application US/09019942

Patent No. 6033855

GENERAL INFORMATION:

APPLICANT: Bertin, John

TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT

TITLE OF INVENTION: DOMAIN POLYPEPTIDES

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FASTSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/019,942

FILING DATE: 06-FEB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Meiklejohn, Ph.D., Anita L.

REGISTRATION NUMBER: 35,283

REFERENCE/DOCKET NUMBER: 07334/068001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1931 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-019-942-2

Query Match 43.8%; Score 731.8; DB 3; Length 1931;
Best Local Similarity 99.7%; Pred. No. 7.6e-165;
Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 331 ACAGTTTACAGAGTGTTCCTCAAGTGCCATTCACCTATGTGCAAGAAAGAAATGGAATATC 390
Db 1149 AAGTTTACAGAGTGTTCCTCAAGTGCCATTCACCTATGTGCAAGAAAGAAATGGAATATC 1208
QY 391 TCTGAACATACCTGTAATCATGCTGCCCAAGAGGAATCATGTGGATCCTCTCAGCTCCA 450
Db 1209 TCTGAACATACCTGTAATCATGCTGCCCAAGAGGAATCATGTGGATCCTCTCAGCTCCA 1268
QY 451 TGAAATATAGTGTTCCTCGAAACTTCAAGGTCCTCCAGGCTCCTCAAGACAAATGATTT 510
Db 1269 TGAAATATAGTGTTCCTCGAAACTTCAAGGTCCTCCAGGCTCCTCAAGACAAATGATTT 1328
QY 511 TTTTACTAGAAAGCTCAAGACGTGTTATTTTATGAAGCTGCATCTCTGATCACAAGACCCAC 570
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QY 691 GCCTGATAGCCAGCAGTGGATCCAGAGCAAAAGGGAGACATTTGTGAACCAATGAC 750
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QY 931 CAAACAAATGGGTCTTTCAGCCTTACCCGGAATATCTTGTGGTTTCTAGATCACCATCTTT 990
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Db 1809 AAATTTACTTCAAAATAAAGCATGTAAAGTGTGCTGTTTTCAGAGAAAGAAATGTTTTCAT 1868
QY 1051 AAAAGGATATTATA 1065
Db 1869 AAAAGGATATTATA 1883

RESULT 4

US-09-099-041A-1

Sequence 1, Application US/09099041A

Patent No. 6340576

GENERAL INFORMATION:

APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/09/099,041A
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)... (1833)
US-09-099-041A-1

Query Match 43.8%; Score 731.8; DB 3; Length 1931;
Best Local Similarity 99.7%; Pred. No. 7.6e-165;
Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 331 ACAGTTACAGAGTGTTCAGTGCCTTCACTATGTGACAGAGAGAAATGGAATTATC 390
DB 1149 AAGTTACAGAGTGTTCAGTGCCTTCACTATGTGACAGAGAGAAATGGAATTATC 1208
QY 391 TCTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGATCTCTCAGCTCCA 450
DB 1209 TCTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGATCTCTCAGCTCCA 1268
QY 451 TGAATAATAGTGTCTCTGAACTTCAAGTCCCTGCGAGCTCCTCAAGACAATGATTT 510
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DB 1749 CAAACAAATGGTCTTCAAGCTTACCGGAATACCTGTGGTTCTAGATCAACATCTTT 1808
QY 991 AAATTTACTTCAAAATTAAGCATGTAGTGAAGTGTGTTTCAAGAGAGAAATGTTTTCAT 1050
DB 1809 AAATTTACTTCAAAATTAAGCATGTAGTGAAGTGTGTTTCAAGAGAGAAATGTTTTCAT 1868
QY 1051 AAAAGATATTATTA 1065

Db 1869 AAAAGATATTATTA 1883
RESULT 5
US-09-245-281-1
; Sequence 1, Application US/09245281
; Patent No. 6369196
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/09/245,281
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: US 09/207,359
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: US 09/099,041
; EARLIER FILING DATE: 1998-06-17
; EARLIER APPLICATION NUMBER: US 09/019,942
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)... (1833)
US-09-245-281-1

Query Match 43.8%; Score 731.8; DB 3; Length 1931;
Best Local Similarity 99.7%; Pred. No. 7.6e-165;
Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 331 ACAGTTACAGAGTGTTCAGTGCCTTCACTATGTGACAGAGAGAAATGGAATTATC 390
DB 1149 AAGTTACAGAGTGTTCAGTGCCTTCACTATGTGACAGAGAGAAATGGAATTATC 1208
QY 391 TCTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGATCTCTCAGCTCCA 450
DB 1209 TCTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGATCTCTCAGCTCCA 1268
QY 451 TGAATAATAGTGTCTCTGAACTTCAAGTCCCTGCGAGCTCCTCAAGACAATGATTT 510
DB 1269 TGAATAATAGTGTCTCTGAACTTCAAGTCCCTGCGAGCTCCTCAAGACAATGATTT 1328
QY 511 TTTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCTGGAAATCA 570
DB 1329 TTTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCTGGAAATCA 1388
QY 571 CAGTTGGATAGACACCATTTCTGGATCTCAAAAGGCTGCATCTGTGATCAAGACCAAC 630
DB 1389 CAGTTGGATAGACACCATTTCTGGATCTCAAAAGGCTGCATCTGTGATCAAGACCAAC 1448
QY 631 TCCATGCTCTTCAAGCAATTAATCCACTCTCAAGTCCCTGCGAGCTCCTCAAGACGCTGCA 690
DB 1449 TCCATGCTCTTCAAGCAATTAATCCACTCTCAAGTCCCTGCGAGCTCCTCAAGACGCTGCA 1508
QY 691 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTAACCAATGAC 750
DB 1509 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTAACCAATGAC 1568
QY 751 AGAAGCTGCTTAAACCATTTCTGGATCTCAAAAGGCTGCATCTGTGATCAAGACCAAC 810
DB 1569 AGAAGCTGCTTAAACCATTTCTGGATCTCAAAAGGCTGCATCTGTGATCAAGACCAAC 1628
QY 811 GCATATGAACTTGTAGTACCAAGCTCAAGGACCTCAAAAGTCAGACCAATTAAGTACA 870
DB 1629 GCATATGAACTTGTAGTACCAAGCTCAAGGACCTCAAAAGTCAGACCAATTAAGTACA 1688
QY 871 CACTACTGACATCCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATAA 930

Db 1689 CACTACTGACATCCAAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAA 1748
QY 931 CAAACAAATGGGTCTTCAGCCTTTACCGGAAATACTTTGTGGTTTCTAGATCACCATCTTT 990
Db 1749 CAAACAAATGGGTCTTCAGCCTTTACCGGAAATACTTTGTGGTTTCTAGATCACCATCTTT 1808
QY 991 AAATTTACTTCAAAATAAAGACATGTAAGTGACTGTTTTCCTCAAGAGAAATGTTTTCAT 1050
Db 1809 AAATTTACTTCAAAATAAAGACATGTAAGTGACTGTTTTCCTCAAGAGAAATGTTTTCAT 1868
QY 1051 AAAAGGATATTATA 1065
Db 1869 AAAAGGATATTATA 1883

RESULT 6

US-09-470-271-2
; Sequence 2, Application US/09470271
; Patent No. 6410689
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
; TITLE OF INVENTION: DOMAIN POLYPEPTIDES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/470,271
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/019,942
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/068001
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1931 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-470-271-2

Query Match 43.8%; Score 731.8; DB 4; Length 1931;
Best Local Similarity 99.7%; Pred. No. 7.6e-165;
Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 331 ACAGTTACAGAGTGTTCAGATGCCATTACCTATGTGACAAAGAAATGGAATATC 390
Db 1149 AAAGTTACAGAGTGTTCAGATGCCATTACCTATGTGACAAAGAAATGGAATATC 1208
QY 391 TCTGAACATACCTGTAAATCATGTCCACAAAGAGGAATCATGTGGATCCCTCTCAGCTCCA 450
Db 1209 TCTGAACATACCTGTAAATCATGTCCACAAAGAGGAATCATGTGGATCCCTCTCAGCTCCA 1268
QY 451 TGAAGATAGTGGTTCTCCTGAAACTTCAAGGTCCTGCCAGCTCCTCAAGACAAATGATTT 510

Db 1269 TGAAGATAGTGGTTCTCCTGAAACTTCAAGGTCCTGCCAGCTCCTCAAGACAAATGATTT 1328
QY 511 TTTATCTAGAAAGCTCAAGACTGTGTTATTTATTAAGAGCTGCATCACTGTCTCTGGAATCA 570
Db 1329 TTTATCTAGAAAGCTCAAGACTGTGTTATTTATTAAGAGCTGCATCACTGTCTCTGGAATCA 1388
QY 571 CAGTTGGGATAGCACCATTCTCGGATCTCAAAAGGCTGCATTTCTGTGATCACAAGACCAC 630
Db 1389 CAGTTGGGATAGCACCATTCTCGGATCTCAAAAGGCTGCATTTCTGTGATCACAAGACCAC 1448
QY 631 TCCATGCTCTTCAGCAATAATAAATCCACTCTCAACTCGAGGAACTCAGAACGCTCTGCA 690
Db 1449 TCCATGCTCTTCAGCAATAATAAATCCACTCTCAACTCGAGGAACTCAGAACGCTCTGCA 1508
QY 691 GCCTGGTATAGCCCGCAGCTGGATCCAGAGCAAAAGGAGAGACATTTGTGAACCAATGAC 750
Db 1509 GCCTGGTATAGCCCGCAGCTGGATCCAGAGCAAAAGGAGAGACATTTGTGAACCAATGAC 1568
QY 751 AGAAGCCTGCTCTTAACCCAGTCGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAAGA 810
Db 1569 AGAAGCCTGCTCTTAACCCAGTCGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAAGA 1628
QY 811 GGAATATGAATCTGTTAGTACCAAGCTCAAGGACTTCAAAAGTCAGACAATTACTAGA 870
Db 1629 GGAATATGAATCTGTTAGTACCAAGCTCAAGGACTTCAAAAGTCAGACAATTACTAGA 1688
QY 871 CACTACTGACATCCAAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAA 930
Db 1689 CACTACTGACATCCAAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAA 1748
QY 931 CAAACAAATGGGTCTTTCAGCCTTTACCCGGAAATACTTTGTGGTTTCTAGATCACCATCTTT 990
Db 1749 CAAACAAATGGGTCTTTCAGCCTTTACCCGGAAATACTTTGTGGTTTCTAGATCACCATCTTT 1808
QY 991 AAATTTACTTCAAAATAAAGACATGTAAGTGACTGTTTTCCTCAAGAGAAATGTTTTCAT 1050
Db 1809 AAATTTACTTCAAAATAAAGACATGTAAGTGACTGTTTTCCTCAAGAGAAATGTTTTCAT 1868
QY 1051 AAAAGGATATTATA 1065
Db 1869 AAAAGGATATTATA 1883

RESULT 7

US-09-207-359B-1
; Sequence 1, Application US/09207359B
; Patent No. 6469140
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/207,359B
; CURRENT FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-09-207-359B-1

Query Match 43.8%; Score 731.8; DB 4; Length 1931;
Best Local Similarity 99.7%; Pred. No. 7.6e-165;
Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

;
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/865,364
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-09-865-364-1

Query Match 43.8%; Score 731.8; DB 4; Length 1931;
Best Local Similarity 99.7%; Pred. No. 7.6e-165;
Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 331 ACAGTTACAGAGTGTTTCAAGTGCCATTACCTATGTGACAAAGAGAAATGGAATTATC 390
DB 1149 AAGATTACAGAGTGTTTCAAGTGCCATTACCTATGTGACAAAGAGAAATGGAATTATC 1208
QY 391 TCTGAACATACCTGTAAATCATGGTCCAAAGAGGAATCATGTGGATCTCTCAGCTCCA 450
DB 1209 TCTGAACATACCTGTAAATCATGGTCCAAAGAGGAATCATGTGGATCTCTCAGCTCCA 1268
QY 451 TGAATAATAGTGTTTCTCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTT 510
DB 1269 TGAATAATAGTGTTTCTCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTT 1328
QY 511 TTATCTAGAAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCTCTGGAATCA 570
DB 1329 TTATCTAGAAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCTCTGGAATCA 1388
QY 571 CAGTTGGGATAGCACCATTCTTGGATCTCAAAGGGCTGCATTTCTGTGATCACAAGACCAC 630
DB 1389 CAGTTGGGATAGCACCATTCTTGGATCTCAAAGGGCTGCATTTCTGTGATCACAAGACCAC 1448
QY 631 TCATGCTCTTCAGCAATATAATCACTCTCAAGGGCTGCATTTCTGTGATCACAAGACCAC 690
DB 1449 TCATGCTCTTCAGCAATATAATCACTCTCAAGGGCTGCATTTCTGTGATCACAAGACCAC 1508
QY 691 GCCTGGTATAGCCAGCAGTGATCCAGAGCAAAAGGAGACATTTGTGAACCAAAATGAC 750
DB 1509 GCCTGGTATAGCCAGCAGTGATCCAGAGCAAAAGGAGACATTTGTGAACCAAAATGAC 1568
QY 751 AGAAGCTGCTTTAACCCAGTCGTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGA 810
DB 1569 AGAAGCTGCTTTAACCCAGTCGTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGA 1628
QY 811 GGAATATGAACCTTGTGTAGTACCAAGCCTCAAGGGCTCAAAAGTCAAGCAATTTACTAGA 870
DB 1629 GGAATATGAACCTTGTGTAGTACCAAGCCTCAAGGGCTCAAAAGTCAAGCAATTTACTAGA 1688
QY 871 CACTACTGACATCCAAAGGAGAAATTTGCCAAGTATATGACAAAATTTGAAGATTA 930
DB 1689 CACTACTGACATCCAAAGGAGAAATTTGCCAAGTATATGACAAAATTTGAAGATTA 1748
QY 931 CAAACAAATGGGTCTTACCGGAAATTTTCCGGAATTTCTAGATCACCATCTTT 990
DB 1749 CAAACAAATGGGTCTTACCGGAAATTTTCCGGAATTTCTAGATCACCATCTTT 1808
QY 991 AAATTTACTTCAAAATAAAGCATGTAAAGTACTGTTTTCAGAGAGAAATGTGTTTCAT 1050
DB 1809 AAATTTACTTCAAAATAAAGCATGTAAAGTACTGTTTTCAGAGAGAAATGTGTTTCAT 1868

QY 1051 AAAAGGATATTTATA 1065
DB 1869 AAAAGGATATTTATA 1883
RESULT 10
US-09-748-537-2
; Sequence 2, Application US/09748537
; Patent No. 6680167
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Chao, Moses V.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILIE AND USES THERE
; FILE REFERENCE: 07334-316001
; CURRENT APPLICATION NUMBER: US/09/748,537
; CURRENT FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-748-537-2
Query Match 43.8%; Score 731.8; DB 4; Length 1931;
Best Local Similarity 99.7%; Pred. No. 7.6e-165;
Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 331 ACAGTTACAGAGTGTTTCAAGTGCCATTACCTATGTGACAAAGAGAAATGGAATTATC 390
DB 1149 AAGATTACAGAGTGTTTCAAGTGCCATTACCTATGTGACAAAGAGAAATGGAATTATC 1208
QY 391 TCTGAACATACCTGTAAATCATGGTCCAAAGAGGAATCATGTGGATCTCTCAGCTCCA 450
DB 1209 TCTGAACATACCTGTAAATCATGGTCCAAAGAGGAATCATGTGGATCTCTCAGCTCCA 1268
QY 451 TGAATAATAGTGTTTCTCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTT 510
DB 1269 TGAATAATAGTGTTTCTCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTT 1328
QY 511 TTATCTAGAAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCTCTGGAATCA 570
DB 1329 TTATCTAGAAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCTCTGGAATCA 1388
QY 571 CAGTTGGGATAGCACCATTCTTGGATCTCAAAGGGCTGCATTTCTGTGATCACAAGACCAC 630
DB 1389 CAGTTGGGATAGCACCATTCTTGGATCTCAAAGGGCTGCATTTCTGTGATCACAAGACCAC 1448
QY 631 TCATGCTCTTCAGCAATATAATCACTCTCAAGGGCTGCATTTCTGTGATCACAAGACCAC 690
DB 1449 TCATGCTCTTCAGCAATATAATCACTCTCAAGGGCTGCATTTCTGTGATCACAAGACCAC 1508
QY 691 GCCTGGTATAGCCAGCAGTGATCCAGAGCAAAAGGAGACATTTGTGAACCAAAATGAC 750
DB 1509 GCCTGGTATAGCCAGCAGTGATCCAGAGCAAAAGGAGACATTTGTGAACCAAAATGAC 1568
QY 751 AGAAGCTGCTTTAACCCAGTCGTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGA 810
DB 1569 AGAAGCTGCTTTAACCCAGTCGTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGA 1628
QY 811 GGAATATGAACCTTGTGTAGTACCAAGCCTCAAGGGCTCAAAAGTCAAGCAATTTACTAGA 870
DB 1629 GGAATATGAACCTTGTGTAGTACCAAGCCTCAAGGGCTCAAAAGTCAAGCAATTTACTAGA 1688
QY 871 CACTACTGACATCCAAAGGAGAAATTTGCCAAGTATATGACAAAATTTGAAGATTA 930
DB 1689 CACTACTGACATCCAAAGGAGAAATTTGCCAAGTATATGACAAAATTTGAAGATTA 1748
QY 931 CAAACAAATGGGTCTTACCGGAAATTTTCCGGAATTTCTAGATCACCATCTTT 990

Db 1749 CAAACAAATGGGTCTTCAAGCTTACCCGGAATACCTGTGGTTCTAGATCACCATCTTT 1808
QY 991 AAATTTACTTCAAAATAAAGCATGTAAGTGACTGTTTTTCAAGAGAAATGGTTTCAT 1050
Db 1809 AAATTTACTTCAAAATAAAGCATGTAAGTGACTGTTTTTCAAGAGAAATGGTTTCAT 1868
QY 1051 AAAAGGATATTATA 1065
Db 1869 AAAAGGATATTATA 1883

RESULT 11

US-09-023-655-684
; Sequence 684, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 684:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1060 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: MPHEMOT03
; CLONE: 445186
; US-09-023-655-684

Query Match 41.7%; Score 695.4; DB 4; Length 1060;
Best Local Similarity 99.7%; Pred. No. 2.8e-156;
Matches 707; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 331 ACAGTTACAGAGTGTTCAGTGCCCATTCACCTATGTGACAGAGAAATGGAATTATC 390
Db 352 AAAGTTACAGAGTGTTCAGTGCCCATTCACCTATGTGACAGAGAAATGGAATTATC 411
QY 391 TCTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCA 450
Db 412 TCTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCA 471

QY 451 TGAATAA- GTGTTTCTCTGAAACTTCAAGTCCCTGCGAGCTCTCTCAAGACAATGATT 509
Db 472 TGAATAA- GTGTTTCTCTGAAACTTCAAGTCCCTGCGAGCTCTCTCAAGACAATGATT 531
QY 510 TTTTATCTAGAAAAGCTCAAGACTCTTATTTTATCAAGCTGCATCACTGTCTCTGGAATC 569
Db 532 TTTTATCTAGAAAAGCTCAAGACTCTTATTTTATCAAGCTGCATCACTGTCTCTGGAATC 591
QY 570 ACAGTTGGGATAGCACCATTCTTGATCTCAAGGGCTGCATCTCTGTGATCAAGACCA 629
Db 592 ACAGTTGGGATAGCACCATTCTTGATCTCAAGGGCTGCATCTCTGTGATCAAGACCA 651
QY 630 CTCCATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAACTCAGAACGTCGTC 689
Db 652 CTCCATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAACTCAGAACGTCGTC 711
QY 690 AGCCTGGTATAGCCCGCAGAGTGGAATCCAGAGCAAAAGGAGACATTTGTGAACCAATGA 749
Db 712 AGCCTGGTATAGCCCGCAGAGTGGAATCCAGAGCAAAAGGAGACATTTGTGAACCAATGA 771
QY 750 CAGAGCCCTGCTTAAACCACTGCTAGATGCCCTTCTGTCAGGAGCTTGATCATGAAG 809
Db 772 CAGAGCCCTGCTTAAACCACTGCTAGATGCCCTTCTGTCAGGAGCTTGATCATGAAG 831
QY 810 AGGACTATGAACCTTCTAGTACCAAGCCTCAAGAGACCTCAAAAGCTCAGACAATTACTAG 869
Db 832 AGGACTATGAACCTTCTAGTACCAAGCCTCAAGAGACCTCAAAAGCTCAGACAATTACTAG 891
QY 870 ACATCTAGCATCCAGAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATA 929
Db 892 ACATCTAGCATCCAGAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATA 951
QY 930 ACACCAAAATGGTCTTCAGCTTACCCGGAATACTTGTGGTTCTAGATCACCATCTT 989
Db 952 ACACCAAAATGGTCTTCAGCTTACCCGGAATACTTGTGGTTCTAGATCACCATCTT 1011
QY 990 TAAATTTACTTCAAAATAAAGCATGTAAAGTACTGTTTTCAGAGA 1038
Db 1012 TAAATTTACTTCAAAATAAAGCATGTAAAGTACTGTTTTCAGAGA 1060

RESULT 12

US-09-099-041A-3
; Sequence 3, Application US/09099041A
; Patent No. 6340576
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/09/099,041A
; CURRENT FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-099-041A-3

Query Match 40.9%; Score 681.8; DB 3; Length 1620;
Best Local Similarity 99.7%; Pred. No. 5.7e-153;
Matches 683; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 331 ACAGTTACAGAGTGTTCAGTGCCCATTCACCTATGTGACAGAGAAATGGAATTATC 390
Db 936 AAAGTTACAGAGTGTTCAGTGCCCATTCACCTATGTGACAGAGAAATGGAATTATC 995
QY 391 TCTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCA 450
Db 996 TCTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCA 1055


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331 ACAGTTACAGAGTGTTCACAGTGCATTCACCTATGTGACAGAGAAAATGGAATTATC 390
936 AAAAGTTACAGAGTGTTCACAGTGCATTCACCTATGTGACAGAGAAAATGGAATTATC 995
391 TCTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGATCCTCTCAGCTCCA 450
996 TCTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGATCCTCTCAGCTCCA 1055
451 TGAATAATAGTGGTTCCTCGAAACTTCAAGGTCCTGCGAGCTCCTCAAGACAATGATTT 510
1056 TGAATAATAGTGGTTCCTCGAAACTTCAAGGTCCTGCGAGCTCCTCAAGACAATGATTT 1115
511 TTTATCTAGAAAAGCTCAAGACTGTTATTTATGAGCTGCATCTCTGGAATCA 570
1116 TTTATCTAGAAAAGCTCAAGACTGTTATTTATGAGCTGCATCTCTGGAATCA 1175
571 CAGTTGGGATAGCACCATTCTCGGATCTCAAAAGGCTGCAATCTGTGATCAACAAGCCAT 630
1176 CAGTTGGGATAGCACCATTCTCGGATCTCAAAAGGCTGCAATCTGTGATCAACAAGCCAT 1235
631 TCCATGCTCTTCAGCAATTAATAATCCACTCTCAACTGCGAGGAACTCAGAACGCTGCA 690
1236 TCCATGCTCTTCAGCAATTAATAATCCACTCTCAACTGCGAGGAACTCAGAACGCTGCA 1295
691 GCTGTATAGCCCGAGTGGATCCAGAGCAAAAGGGAAGACATTTGTAACCAATGAC 750
1296 GCTGTATAGCCCGAGTGGATCCAGAGCAAAAGGGAAGACATTTGTAACCAATGAC 1355
751 AGAAGCCTGCTTAAACAGCTGCTAGATGCCCTTCTGTCCAGGGAATTCATGATGAAAGA 810
1356 AGAAGCCTGCTTAAACAGCTGCTAGATGCCCTTCTGTCCAGGGAATTCATGATGAAAGA 1415
811 GGACTATGAACCTTTAGTACCAAGCCTACAGGCTCAAAAGTCAAGATTAATGAAAGATAA 930
1416 GGACTATGAACCTTTAGTACCAAGCCTACAGGCTCAAAAGTCAAGATTAATGAAAGATAA 1535
931 CAAACAAATGGGTCTTCAGCCTTACCGGAAATACCTGTGGTTCTAGATCACCATCTTT 990
1536 CAAACAAATGGGTCTTCAGCCTTACCGGAAATACCTGTGGTTCTAGATCACCATCTTT 1595
991 AAATTTACTTCAAAATAAAGCATG 1015
1596 AAATTTACTTCAAAATAAAGCATG 1620

RESULT 15
US-09-340-620A-3
; Sequence 3, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340, 620A
; CURRENT FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
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ORGANISM: Homo sapiens
US-09-340-620A-3

Query Match 40.9%; Score 681.8; DB 4; Length 1620;
Best Local Similarity 99.7%; Pred. No. 5.7e-153;
Matches 683; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 331 ACAGTTACAGAGTGTTCACAGTGCATTCACCTATGTGACAGAGAAAATGGAATTATC 390
DB 936 AAAAGTTACAGAGTGTTCACAGTGCATTCACCTATGTGACAGAGAAAATGGAATTATC 995
QY 391 TCTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGATCCTCTCAGCTCCA 450
DB 996 TCTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGATCCTCTCAGCTCCA 1055
QY 451 TGAATAATAGTGGTTCCTCGAAACTTCAAGGTCCTGCGAGCTCCTCAAGACAATGATTT 510
DB 1056 TGAATAATAGTGGTTCCTCGAAACTTCAAGGTCCTGCGAGCTCCTCAAGACAATGATTT 1115
QY 511 TTTATCTAGAAAAGCTCAAGACTGTTATTTATGAGCTGCATCTCTGGAATCA 570
DB 1116 TTTATCTAGAAAAGCTCAAGACTGTTATTTATGAGCTGCATCTCTGGAATCA 1175
QY 571 CAGTTGGGATAGCACCATTCTCGGATCTCAAAAGGCTGCAATCTGTGATCAACAAGCCAT 630
DB 1176 CAGTTGGGATAGCACCATTCTCGGATCTCAAAAGGCTGCAATCTGTGATCAACAAGCCAT 1235
QY 631 TCCATGCTCTTCAGCAATTAATAATCCACTCTCAACTGCGAGGAACTCAGAACGCTGCA 690
DB 1236 TCCATGCTCTTCAGCAATTAATAATCCACTCTCAACTGCGAGGAACTCAGAACGCTGCA 1295
QY 691 GCTGTATAGCCCGAGTGGATCCAGAGCAAAAGGGAAGACATTTGTAACCAATGAC 750
DB 1296 GCTGTATAGCCCGAGTGGATCCAGAGCAAAAGGGAAGACATTTGTAACCAATGAC 1355
QY 751 AGAAGCCTGCTTAAACAGCTGCTAGATGCCCTTCTGTCCAGGGAATTCATGATGAAAGA 810
DB 1356 AGAAGCCTGCTTAAACAGCTGCTAGATGCCCTTCTGTCCAGGGAATTCATGATGAAAGA 1415
QY 811 GGACTATGAACCTTTAGTACCAAGCCTACAGGCTCAAAAGTCAAGATTAATGAAAGATAA 930
DB 1416 GGACTATGAACCTTTAGTACCAAGCCTACAGGCTCAAAAGTCAAGATTAATGAAAGATAA 1535
QY 931 CAAACAAATGGGTCTTCAGCCTTACCGGAAATACCTGTGGTTCTAGATCACCATCTTT 990
DB 1536 CAAACAAATGGGTCTTCAGCCTTACCGGAAATACCTGTGGTTCTAGATCACCATCTTT 1595
QY 991 AAATTTACTTCAAAATAAAGCATG 1015
DB 1596 AAATTTACTTCAAAATAAAGCATG 1620
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Search completed: January 31, 2005, 23:09:49
Job time : 168 secs

1 ACCAGGTTATATACCCAGATATTTCTATATTTATATAGGCTCTATCTAGAACCATCTGCGCA 600

QY 61 TGTAGTAATGTTAGATTTCAAGATGAAGCTCTGAGACACTGAGAGAGGTAACCAAT 120
DB 61 TGTAGTAATGTTAGATTTCAAGATGAAGCTCTGAGACACTGAGAGAGGTAACCAAT 120
QY 121 TAAATGAGCCAGGATTCAGAGTCTGTGGTTCCTGAGGTTATTTCCCGTCTACACTGTC 180
DB 121 TAAATGAGCCAGGATTCAGAGTCTGTGGTTCCTGAGGTTATTTCCCGTCTACACTGTC 180
QY 181 TTTTCTCTCAGTTATATGTTATATTTCAACTCTTTATATTTCTTTCCATGATTTTGT 240
DB 181 TTTTCTCTCAGTTATATGTTATATTTCAACTCTTTATATTTCTTTCCATGATTTTGT 240
QY 241 ACAACATATAAATGTTAGATTTATTTTCACTCTATATTTCTCTAATCATCTCCAG 300
DB 241 ACAACATATAAATGTTAGATTTATTTTCACTCTATATTTCTCTAATCATCTCCAG 300
QY 301 TTAAGTGTATATATTTATGTTATTTCACTCTATATTTCTCTAAGTGCCATTC 360
DB 301 TTAAGTGTATATATTTATGTTATTTCACTCTATATTTCTCTAAGTGCCATTC 360
QY 361 CCTATGTGACAGAGAAATGGAATTTCTCTGAAACATACCTGTAAATCATGGTCCACA 420
DB 361 CCTATGTGACAGAGAAATGGAATTTCTCTGAAACATACCTGTAAATCATGGTCCACA 420
QY 421 AGAGGAATCATGTGGATCTCTCAGCTCCATGAAATAGTGTCTCTGAAACTTCAAG 480
DB 421 AGAGGAATCATGTGGATCTCTCAGCTCCATGAAATAGTGTCTCTGAAACTTCAAG 480
QY 481 GTCCCTGCCAGCTCTCAGACAAATGATTTTATCTGAAAGCTCAAGACTGTTATTT 540
DB 481 GTCCCTGCCAGCTCTCAGACAAATGATTTTATCTGAAAGCTCAAGACTGTTATTT 540
QY 541 TATGAAGCTGCATCACTGCTGGAATCACAGTTGGGATAGCACATTTCTGGATCTCA 600
DB 541 TATGAAGCTGCATCACTGCTGGAATCACAGTTGGGATAGCACATTTCTGGATCTCA 600
QY 601 AAGGCTGTGATCTGTGATCACAGACCACTCCATGCTCTTCAAGTAATTAATCCACT 660
DB 601 AAGGCTGTGATCTGTGATCACAGACCACTCCATGCTCTTCAAGTAATTAATCCACT 660
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DB 721 CAAAAGGGAAGACATTTGTAACCAATGACAGAGCTGCTTAACTGCTGATGCTG 780
QY 781 CCTTCTGTCAGGACTTGTATCATGAAGAGGACTATGAATGTTAGTACCAAGCTAC 840
DB 781 CCTTCTGTCAGGACTTGTATCATGAAGAGGACTATGAATGTTAGTACCAAGCTAC 840
QY 841 AAGGACTCAAAAGTCAAGAAATTTACTAGACACTACTGACATCCAAAGGAGAAATTCG 900
DB 841 AAGGACTCAAAAGTCAAGAAATTTACTAGACACTACTGACATCCAAAGGAGAAATTCG 900
QY 901 CAAAGTTATAGTACAAAATTTGAAGATAACAAATGGGTCTTCAGCCTTACCCGA 960
DB 901 CAAAGTTATAGTACAAAATTTGAAGATAACAAATGGGTCTTCAGCCTTACCCGA 960
QY 961 AATCTTGTGGTCTTAGATCACATCTTTTAAATTTACTTCAAAATAAAGCATGTAAGT 1020
DB 961 AATCTTGTGGTCTTAGATCACATCTTTTAAATTTACTTCAAAATAAAGCATGTAAGT 1020
QY 1021 GACTGTTTTCAAGAGAAATGTTTCAATAAAGGATATTTATCTCTGTTGCTTTGA 1080
DB 1021 GACTGTTTTCAAGAGAAATGTTTCAATAAAGGATATTTATCTCTGTTGCTTTGA 1080
QY 1081 CTTTTTTTATATAAATCCGTGAGTATAAGCTTTTATGAAGTCTTTGGGTAATAT 1140
DB 1081 CTTTTTTTATATAAATCCGTGAGTATAAAGCTTTTATGAAGTCTTTGGGTAATAT 1140

QY 1141 TAGTCTCCCTCATGACACTGACATATTTTTTAAATTAATACAGTAAAGTTTGAAT 1200
DB 1141 TAGTCTCCCTCATGACACTGACATATTTTTTAAATTAATACAGTAAAGTTTGAAT 1200
QY 1201 TTTGCTACATAGTTCAATTTTTTATGTCCTTTTAAACAGAAACCACTTTTAAAGGATA 1260
DB 1201 TTTGCTACATAGTTCAATTTTTTATGTCCTTTTAAACAGAAACCACTTTTAAAGGATA 1260
QY 1261 GTAAATATCTTGTGTTTATAACAGTGCCTTAAAGGTATGATGATTTCTGATGGAAGCCATT 1320
DB 1261 GTAAATATCTTGTGTTTATAACAGTGCCTTAAAGGTATGATGATTTCTGATGGAAGCCATT 1320
QY 1321 TTCACTATCATGTTCTTCACTGATTTTGTCTTAAAGTCTGATGATTTTAT 1380
DB 1321 TTCACTATCATGTTCTTCACTGATTTTGTCTTAAAGTCTGATGATTTTAT 1380
QY 1381 GAAGTATATACCTTTTACCCACAGACAGTACAGAAATCCCTGCTTAAATCCAGGC 1440
DB 1381 GAAGTATATACCTTTTACCCACAGACAGTACAGAAATCCCTGCTTAAATCCAGGC 1440
QY 1441 TTAATGCTTACAAAGGTTTAAATTTAAACCTCAATTTAGGATTAATTTTAAAG 1500
DB 1441 TTAATGCTTACAAAGGTTTAAATTTAAACCTCAATTTAGGATTAATTTTAAAG 1500
QY 1501 TTTTATTTATGATTTCCCTTTTAAATGATATTTTCAAGGTAAACATATAAAG 1560
DB 1501 TTTTATTTATGATTTCCCTTTTAAATGATATTTTCAAGGTAAACATATAAAG 1560
QY 1561 AAAAAATTAATATATTAATACCGCTTCTGTCCTTAACTTAACTCAGCTTCCCTA 1620
DB 1561 AAAAAATTAATATATTAATACCGCTTCTGTCCTTAACTTAACTCAGCTTCCCTA 1620
QY 1621 CTGTGACCAACCAACCAAGCTAAATAAGTCAACAGCTGATGTGTAATA 1669
DB 1621 CTGTGACCAACCAACCAAGCTAAATAAGTCAACAGCTGATGTGTAATA 1669

RESULT 2

US-09-925-301-173
; Sequence 173, Application US/09925301
; Patent No. US2002052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 173
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2595)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (2622)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (2659)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (2670)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-173

Query Match

79.8%; Score 1332.4; DB 9; Length 2709;

Best Local Similarity 99.6%; Pred. No. 1.4e-269; Matches 1330; Conservative 5; Mismatches 1; Indels 0; Gaps 0;			
QY	331	ACAGTTTACAGAGTGTTCCTCAAGTGCCCATTCACCTATCTGTGACCAAGAGAAAATGGAATTATC	390
Db	1202	AAAGTTTACAGAGTGTTCCTCAAGTGCCCATTCACCTATCTGTGACCAAGAGAAAATGGAATTATC	1261
QY	391	TCTGAACATACCTGTAAATCATGGTCCCAAGAGGAAATCATGTGGATCCTCTCAGCTCCA	450
Db	1262	TCTGAACATACCTGTAAATCATGGTCCCAAGAGGAAATCATGTGGATCCTCTCAGCTCCA	1321
QY	451	TGAAATAGTGGTTCCTCGAAACTTCAAGGTCCTCCAGGTCCTCTCAAGACAAATGATTT	510
Db	1322	TGAAATAGTGGTTCCTCGAAACTTCAAGGTCCTCCAGGTCCTCTCAAGACAAATGATTT	1381
QY	511	TTTATCTAGAAAAGCTCAAGACTGTGTTATTTATGAAGCTGTCATCAGTGCCTGGAATCA	570
Db	1382	TTTATCTAGAAAAGCTCAAGACTGTGTTATTTATGAAGCTGTCATCAGTGCCTGGAATCA	1441
QY	571	CAGTTGGGATAGCACCAATTTCTGGAATCTCAAGGGCTGCAATCTGTGATCACAAGACCAC	630
Db	1442	CAGTTGGGAYAGCACCAATTTCTGGAATCTCAAGGGCTGCAATCTGTGATCACAAGACCAC	1501
QY	631	TCCATGCTCTTACGCAATTAATAATCCACTCTCAACTGCGAGAAATCTCAGAACTGTGCA	690
Db	1502	TCCATGCTCTTACGCAATTAATAATCCACTCTCAACTGCGAGAAATCTCAGAACTGTGCA	1561
QY	691	GCTGTGTATAGCCACGAGTGGATCCAGAGCAAAAGGGAGACATTTGCAACCAATGAC	750
Db	1562	GCTGTGTATAGCCACGAGTGGATCCAGAGCAAAAGGGAGACATTTGCAACCAATGAC	1621
QY	751	AGAAGCTGCTCTTAACAGCTGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAAGA	810
Db	1622	AGAAGCTGCTCTTAACAGCTGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAAGA	1681
QY	811	GGACTATGAACCTTGTAGTACCAAGCTCAAGGACTCAAAAGTCAGACAAATTACTAGA	870
Db	1682	GGACTATGAACCTTGTAGTACCAAGCTCAAGGACTCAAAAGTCAGACAAATTACTAGA	1741
QY	871	CACCTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAA	930
Db	1742	CACCTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAA	1801
QY	931	CAAAACAAATGGGTCTTTCAGCTTTACCCGGAAATACCTTGTGGTTTCTAGATCACCATCTTT	990
Db	1802	CAAAACAAATGGGTCTTTCAGCTTTACCCGGAAATACCTTGTGGTTTCTAGATCACCATCTTT	1861
QY	991	AAATTTACTTTCAAAATAAAGCATGTAAGTACTGTTTTTCAAGAGAAATGTTGTTTCAT	1050
Db	1862	AAATTTACTTTCAAAATAAAGCATGTAAGTACTGTTTTTCAAGAGAAATGTTGTTTCAT	1921
QY	1051	AAAAGGATATTTATATCTCTGTGCTTTCAGCTTTTATATAAATCCGTGAGTATTA	1110
Db	1922	AAAAGGATATTTATATCTCTGTGCTTTCAGCTTTTATATAAATCCGTGAGTATTA	1981
QY	1111	AGCTTTATTAAGGTTCTTTGGGTAATATTAAGTCTCCCTCCATGACACTGCAAGTATTTT	1170
Db	1982	AGCTTTATTAAGGTTCTTTGGGTAATATTAAGTCTCCCTCCATGACACTGCAAGTATTTT	2041
QY	1171	TTTTTAATTAACAAGTAAAGTTTGAATTTTGTCTACATAGTTCATTTTATGTCCT	1230
Db	2042	TTTTTAATTAACAAGTAAAGTTTGAATTTTGTCTACATAGTTCATTTTATGTCCT	2101
QY	1231	TTTGTAAACAGAACCACTTTAAAGATAGTAAATTTCTGTTTATTAACAGTGCCTTA	1290
Db	2102	TTTGTAAACAGAACCACTTTAAAGATAGTAAATTTCTGTTTATTAACAGTGCCTTA	2161
QY	1291	AGGTATGATGTTTCTGTGAGGAGCAATTTTCACATTCATGTTCTTCTGATGATTTTGG	1350
Db	2162	AGGTATGATGTTTCTGTGAGGAGCAATTTTCACATTCATGTTCTTCTGATGATTTTGG	2221
QY	1351	TTACTTGTCTAAGATGCAATTTGATTTTATGAAGTATATACCCCTTTACCCACAGAGACA	1410

Db	2222	TTACTTGKCTAARAWCAATTTGATTTTATGAAGTATATACCCCTTTACCCACAGAGACA	2281
QY	1411	GTACAGAAATCCCTGCCCTAAAAATCCAGGCTTAAATTTGCCCTTACAAAGGGTTATTAATTTA	1470
Db	2282	GTACAGAAATCCCTGCCCTAAAAATCCAGGCTTAAATTTGCCCTTACAAAGGGTTATTAATTTA	2341
QY	1471	AAATCCCAATTTATAGATTTACATTTTAAAGTTTATTTATGAATTTCCCTTTAAAAATGAT	1530
Db	2342	AAATCCCAATTTATAGATTTACATTTTAAAGTTTATTTATGAATTTCCCTTTAAAAATGAT	2401
QY	1531	ATTTCCAAAGGTAAACCAATACAAATTAAGAAAGAAATAAATATATATATATACCGGCTTCC	1590
Db	2402	ATTTCCAAAGGTAAACCAATACAAATTAAGAAAGAAATAAATATATATATATACCGGCTTCC	2461
QY	1591	TGTCCTCCATTTTAACTCCAGCTTCCCTTACTGTCAACCAACCAAGCTAAATAAAGTC	1650
Db	2462	TGTCCTCCATTTTAACTCCAGCTTCCCTTACTGTCAACCAACCAAGCTAAATAAAGTC	2521
QY	1651	AACAGCCTGATGTGA 1666	
Db	2522	AACAGCCTGATGTGA 2537	
RESULT 3			
US-09-981-397A-13			
; Sequence 13, Application US/09981397A			
; Publication No. US20030082519A1			
; GENERAL INFORMATION:			
; APPLICANT: Axxima Pharmaceuticals AG			
; APPLICANT: Schubart, Daniel			
; APPLICANT: Habenberger, Peter			
; APPLICANT: Stein-Gerlach, Matthias			
; APPLICANT: Bevec, Dorian			
; TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their			
; TITLE OF INVENTION: Inhibition			
; FILE REFERENCE: AXM-004.1 US			
; CURRENT APPLICATION NUMBER: US/09/981,397A			
; PRIOR FILING DATE: 2002-06-28			
; PRIOR APPLICATION NUMBER: 60/240,750			
; PRIOR FILING DATE: 2000-10-16			
; NUMBER OF SEQ ID NOS: 22			
; SOFTWARE: Patentin version 3.1			
; SEQ ID NO 13			
; LENGTH: 2501			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-981-397A-13			
Query Match 78.4%; Score 1308; DB 10; Length 2501;			
Best Local Similarity 99.0%; Pred. No. 1.8e-264;			
Matches 1329; Conservative 0; Mismatches 5; Indels 8; Gaps 1;			
QY	331	ACAGTTACAGAGTGTTCAGTGCCTTCCATTCACCTATGTGTGACCAAGAAAATGGAATTATC	390
Db	1160	AAAGTTACAGAGTGTTCAGTGCCTTCCATTCACCTATGTGTGACCAAGAAAATGGAATTATC	1219
QY	391	TCGTGACATACCTGTAAATCATGTGTCCCAAGAGGAATCATGTGGATCTCTCAGCTCCA	450
Db	1220	TCGTGACATACCTGTAAATCATGTGTCCCAAGAGGAATCATGTGGATCTCTCAGCTCCA	1279
QY	451	TGAAATAGTGGTTCCTCTGAAACTTCAAGGTCCTCCAGCTCTCTCAAGACAATGATTT	510
Db	1280	TGAAATAGTGGTTCCTCTGAAACTTCAAGGTCCTCCAGCTCTCTCAAGACAATGATTT	1339
QY	511	TTTATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCCTGCTGGAATCA	570
Db	1340	TTTATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCCTGCTGGAATCA	1399
QY	571	CAGTTGGGATAGCACCATTTCTGGGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCAC	630
Db	1400	CAGTTGGGATAGCACCATTTCTGGGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCAC	1459
QY	631	TCCATGCTCTTACGCAATTAATAATCCACTCTCAACTGCAGGAAACTCAGAACGCTGTGCA	690

Db 1460 TCCATGCTCTTCAGCAATAATAATATCCCACTCTCACTCAGAGAACTCAGAACGCTCTGCA 1519
QY 691 GCCTGGTATAGCCAGCAGTGTATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 750
Db 1520 GCCTGGTATAGCCAGCAGTGTATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGAC 1579
QY 751 AGAGCCTGCTTAAACCAAGTCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGA 810
Db 1580 AGAGCCTGCTTAAACCAAGTCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGA 1639
QY 811 GCATATGAACCTTTAGTACCAAGCTACAGAGCACTCAAAAGTCAGCAATTTACTAGA 870
Db 1640 GCATATGAACCTTTAGTACCAAGCTACAGAGCACTCAAAAGTCAGCAATTTACTAGA 1699
QY 871 CACTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAA 930
Db 1700 CACTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAA 1759
QY 931 CAAAAGATGGGTCTTCAGCCTTACCCGGAATACCTTGTGGTTCCTAGATCACCATCTTT 990
Db 1760 CAAAAGATGGGTCTTCAGCCTTACCCGGAATACCTTGTGGTTCCTAGATCACCATCTTT 1819
QY 991 AATTTACTTCAAAATATAAGCATGTAGTGAATTTTCAAGAGAAATGTGTTTCAT 1050
Db 1820 AATTTACTTCAAAATATAAGCATGTAGTGAATTTTCAAGAGAAATGTGTTTCAT 1879
QY 1051 AAAAGGATATTTATCTCTGTGCTTGCATTTTTTATATAAAATCCGTGAGTATTA 1110
Db 1880 AAAAGGATATTTATCTCTGTGCTTGCATTTTTTATATAAAATCCGTGAGTATTA 1939
QY 1111 AGCTTTATGAAGTCTTTGGTAAATTTAGTCTCCCTCATGACACTGAGTATTT 1170
Db 1940 AGCTTTATGAAGTCTTTGGTAAATTTAGTCTCCCTCATGACACTGAGTATTT 1999
QY 1171 TTTTAAATTAATCAAGTAAAAAGTT-----TGAATTTTGTCTACATAGTTCAATTTTT 1222
Db 2000 TTTTAAATTAATCAAGTAAAAAGTTGAAATTTGTTGAAATTTGCTACATAGTTCAATTTTT 2059
QY 1223 ATGTCTCTTTTGTAAAGAACCACTTTTAAAGGATAGTAATTTCTTGTGTTTAAACA 1282
Db 2060 ATGTCTCTTTTGTAAAGAACCACTTTTAAAGGATAGTAATTTCTTGTGTTTAAACA 2119
QY 1283 GTGCCCTTAAGGATAGTATTTCTCATGAGGCCATTTTCACTTCATGTTCTTCATGG 1342
Db 2120 GTGCCCTTAAGGATAGTATTTCTCATGAGGCCATTTTCACTTCATGTTCTTCATGG 2179
QY 1343 ATTAATTTGTACTTGTCTAAGATGCAATTTGATTTTATGAAGTATATACCCCTTACCCAC 1402
Db 2180 ATTAATTTGTACTTGTCTAAGATGCAATTTGATTTTATGAAGTATATACCCCTTACCCAC 2239
QY 1403 CAGAGACAGTACAGATCCCTGCCCTTAAATCCAGGCTTAATTCGCCCTACAAAGGTTA 1462
Db 2240 CAGAGACAGTACAGATCCCTGCCCTTAAATCCAGGCTTAATTCGCCCTACAAAGGTTA 2299
QY 1463 TTAATTTAAACCTCAATTTATAGATTTACATTTTAAAGTTTATTTATGAATTTCCCTTTA 1522
Db 2300 TTAATTTAAACCTCAATTTATAGATTTACATTTTAAAGTTTATTTATGAATTTCCCTTTA 2359
QY 1523 AAAATGATATTTCAAAGGTAAAAACAATACAAATAAAGAAAAAATAATATATTAATAC 1582
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QY 1583 CGGCTTCTGTCGCCATTTTAACTTACCTCAGCTTCCCTACTGTCCCAACCAACCAAGCTAA 1642
Db 2420 CGGCTTCTGTCGCCATTTTAACTTACCTCAGCTTCCCTACTGTCCCAACCAACCAAGCTAA 1699
QY 1643 ATAAAGTCAACAGCTGATGTG 1664
Db 2480 ATAAAGTCAACAGCTGATGTG 2501

US-10-825-282-35
; Sequence 35, Application US/10825282
; Publication No. US20040224389A1
; GENERAL INFORMATION:
; APPLICANT: 3921-1-1-1
; TITLE OF INVENTION: VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3921-1-1-1
; CURRENT APPLICATION NUMBER: US/10/825,282
; CURRENT FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/456,357
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: 60/134,416
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 09/087,195
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 08/378,507
; PRIOR FILING DATE: 1995-01-26
; PRIOR APPLICATION NUMBER: 08/250,478
; PRIOR FILING DATE: 1994-05-27
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 35
; LENGTH: 2501
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (225)..(1847)
US-10-825-282-35

Query Match 78.4%; Score 1308; DB 18; Length 2501;
Best Local Similarity 99.0%; Pred. No. 1.8e-264;
Matches 1329; Conservative 0; Mismatches 5; Indels 8; Gaps 1;
QY 331 ACAGTTACAGAGTGTTCAGAGTGCATTCACCTATGTGACAGAGAAATGGAATTTATC 390
Db 1160 AAGTTACAGAGTGTTCAGAGTGCATTCACCTATGTGACAGAGAAATGGAATTTATC 1219
QY 391 TCTGACATACCTGTAAATCATGTGCCAAGAGAAATCATGTGATCCTCTCAGCTCCA 450
Db 1220 TCTGACATACCTGTAAATCATGTGCCAAGAGAAATCATGTGATCCTCTCAGCTCCA 1279
QY 451 TGAATAATAGTGTTCCTCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTT 510
Db 1280 TGAATAATAGTGTTCCTCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTT 1339
QY 511 TTTATCTAGAAAAGCTCAAGACTGTTATTTTATGAGCTGCATCACTCTCTGGAATCA 570
Db 1340 TTTATCTAGAAAAGCTCAAGACTGTTATTTTATGAGCTGCATCACTCTCTGGAATCA 1399
QY 571 CAGTTGGGATAGCACCATTCTTGGATCTCAAGGGCTGCATTTCTGTGATCAAGACCCAC 630
Db 1400 CAGTTGGGATAGCACCATTCTTGGATCTCAAGGGCTGCATTTCTGTGATCAAGACCCAC 1459
QY 631 TCCATGCTCTTCCAGCAATAATAATCCACTCTCACTCAGGAACTCAGAACGCTGCA 690
Db 1460 TCCATGCTCTTCCAGCAATAATAATCCACTCTCACTCAGGAACTCAGAACGCTGCA 1519
QY 691 GCCTGGTATAGCCAGCAGTGTATCCAGAGCAAAAGGGAAGACATTTGAAACCAATGAC 750
Db 1520 GCCTGGTATAGCCAGCAGTGTATCCAGAGCAAAAGGGAAGACATTTGAAACCAATGAC 1579
QY 751 AGAGCCTGCTTAAACCAAGTCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGA 810
Db 1580 AGAGCCTGCTTAAACCAAGTCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGA 1639
QY 811 GCATATGAACCTTTAGTACCAAGCTACAGAGCACTCAAAAGTCAGCAATTTACTAGA 870
Db 1640 GCATATGAACCTTTAGTACCAAGCTACAGAGCACTCAAAAGTCAGCAATTTACTAGA 1699
QY 871 CACTACTGACATCCAAAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAA 930

Db 1700 CACTACTGACATCCAAAGGAGAGAAATTTGCAAGATTATAGTACAAAAATTGAAGATAA 1759
QY 931 CAAACAAATGGGTCTTCAGCCTTACCCGGAAATACCTGTGGTTTCTAGATCACCATCTTT 990
Db 1760 CAAACAAATGGGTCTTCAGCCTTACCCGGAAATACCTGTGGTTTCTAGATCACCATCTTT 1819
QY 991 AAATTTACTTCAAAATAAAGCATGTAAAGTACTGTTTTCAGAGAAATGTTGTTTCAT 1050
Db 1820 AAATTTACTTCAAAATAAAGCATGTAAAGTACTGTTTTCAGAGAAATGTTGTTTCAT 1879
QY 1051 AAAAGGATATTTATATCTCTGTGCTTTCAGCTTTTATATATAAATCCGTGAGTATTA 1110
Db 1880 AAAAGGATATTTATATCTCTGTGCTTTCAGCTTTTATATATAAATCCGTGAGTATTA 1939
QY 1111 AGCTTTATTCAAGGTTCTTTGGTAAATATTAGTCTCCCTCCATGACATGCAAGTATTTT 1170
Db 1940 AGCTTTATTCAAGGTTCTTTGGTAAATATTAGTCTCCCTCCATGACATGCAAGTATTTT 1999
QY 1171 TTTTAATTAAATCAAGTAAAGTT-----TGAATTTTGCTACATGTTCAATTTT 1222
Db 2000 TTTTAATTAAATCAAGTAAAGTTGAAATTTGTTGCAATTTGCTACATGTTCAATTTT 2059
QY 1223 ATGCTCTTTTGTACAGAAACCACTTTTAAAGGATAGTAAATTTCTGTTTATAACA 1282
Db 2060 ATGCTCTTTTGTACAGAAACCACTTTTAAAGGATAGTAAATTTCTGTTTATAACA 2119
QY 1283 GTGCCCTTAAGGTATGATGATTTCTGATGGAAGCCATTTTCAATTCATGTTCTTCATGG 1342
Db 2120 GTGCCCTTAAGGTATGATGATTTCTGATGGAAGCCATTTTCAATTCATGTTCTTCATGG 2179
QY 1343 ATTATTGTTTACTGTTCTAAGATGCAATTTGATTTTATGAAGTATATACCTTTACCCAC 1402
Db 2180 ATTATTGTTTACTGTTCTAAGATGCAATTTGATTTTATGAAGTATATACCTTTACCCAC 2239
QY 1403 CAGAGACGTACAGATCCCTGCTCCCTAAATCCAGGCTTAATTTGCCCTACAAGGTTA 1462
Db 2240 CAGAGACGTACAGATCCCTGCTCCCTAAATCCAGGCTTAATTTGCCCTACAAGGTTA 2299
QY 1463 TTAATTTAAATCCCAATTATTAGATTAATTTTAAAGTTTATTTATGAATTTCCCTTTA 1522
Db 2300 TTAATTTAAATCCCAATTATTAGATTAATTTTAAAGTTTATTTATGAATTTCCCTTTA 2359
QY 1523 AAATGATATTTCAAAGGTAAACAATAACAATAAAGAAATAAATAATATATTAATAC 1582
Db 2360 AAATGATATTTCAAAGGTAAACAATAACAATAAAGAAATAAATAATATATTAATAC 2419
QY 1583 CGGCTTCTGTCCTCCATTTTAACTTCCCTCAGCTTCCCTACTGTCACCAACAACCAAGCTAA 1642
Db 2420 CGGCTTCTGTCCTCCATTTTAACTTCCCTCAGCTTCCCTACTGTCACCAACAACCAAGCTAA 2479
QY 1643 ATAAAGTCAACAGCCTGATGTG 1664
Db 2480 ATAAAGTCAACAGCCTGATGTG 2501

RESULT 5
US-09-748-537-2
; Sequence 2, Application US/09748537
; Patent No. US20020061833A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Chao, Moses V.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILIE AND USES THERE
; FILE REFERENCE: 07334-316001
; CURRENT APPLICATION NUMBER: US/09/748,537
; CURRENT FILING DATE: 2000-12-26
; PRIOR FILING DATE: 1998-06-17
; PRIOR FILING DATE: 1998-06-17
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2

; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-748-537-2
Query Match 43.8%; Score 731.8; DB 9; Length 1931;
Best Local Similarity 99.7%; Pred. No. 1.9e-143;
Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 331 ACAGTTTACAGAGTGTGTTTCAAGTGCCATTCACCTATGTGCAAGAGAAATGGAATATC 390
Db 1149 AAAGTTTACAGAGTGTGTTTCAAGTGCCATTCACCTATGTGCAAGAGAAATGGAATATC 1208
QY 391 TCTGAACATACCTGTAAATCATGTTCCACAAGAGGAATCATGTGGAATCTCTCAGCTCCA 450
Db 1209 TCTGAACATACCTGTAAATCATGTTCCACAAGAGGAATCATGTGGAATCTCTCAGCTCCA 1268
QY 451 TGAATAATAGTGTGTTCTCTGAAACCTTCAAGGTCCCTGCCAGCTCCTCAAGACAAATGATTT 510
Db 1269 TGAATAATAGTGTGTTCTCTGAAACCTTCAAGGTCCCTGCCAGCTCCTCAAGACAAATGATTT 1328
QY 511 TTTATCTAGAAAAGCTCAAGACTGTTTATTTTATGAAGCTGCATCTCTGATCAAGAACCA 570
Db 1329 TTTATCTAGAAAAGCTCAAGACTGTTTATTTTATGAAGCTGCATCTCTGATCAAGAACCA 1388
QY 571 CAGTTGGGATAGCACCATTTCTGGATCTCAAAAGGGCTGCAATTTCTGTGATCAAGAACCA 630
Db 1389 CAGTTGGGATAGCACCATTTCTGGATCTCAAAAGGGCTGCAATTTCTGTGATCAAGAACCA 1448
QY 631 TCCATGCTCTTTCAGCAATAATAATCACTCTCAACTGAGGAACTCAAGAGCTGCA 690
Db 1449 TCCATGCTCTTTCAGCAATAATAATCACTCTCAACTGAGGAACTCAAGAGCTGCA 1508
QY 691 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGCAACCAATGAC 750
Db 1509 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGCAACCAATGAC 1568
QY 751 AGAAGCTCGCTTAAACAGTCGTAGATGCCCTTCTGTCCAGGACTTGCATCATGAAAGA 810
Db 1569 AGAAGCTCGCTTAAACAGTCGTAGATGCCCTTCTGTCCAGGACTTGCATCATGAAAGA 1628
QY 811 GGACTATGAATCTTTAGTACCAAGCTTCAAGGACTCAAGAGCTCAAGAGTCAAGTACTAGA 870
Db 1629 GGACTATGAATCTTTAGTACCAAGCTTCAAGGACTCAAGAGCTCAAGAGTCAAGTACTAGA 1688
QY 871 CACTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAATTTGAAGATAA 930
Db 1689 CACTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAATTTGAAGATAA 1748
QY 931 CAAACAAATGGGTCTTTCAGCCTTACCCGGAATACTTTGGTTTCTAGATCACCATCTTT 990
Db 1749 CAAACAAATGGGTCTTTCAGCCTTACCCGGAATACTTTGGTTTCTAGATCACCATCTTT 1808
QY 991 AAATTTACTTCAAAATAAAGCATGTAAAGTACTGTTTTCAGAGAAATGTTGTTTCAT 1050
Db 1809 AAATTTACTTCAAAATAAAGCATGTAAAGTACTGTTTTCAGAGAAATGTTGTTTCAT 1868
QY 1051 AAAAGGATATTTATA 1065
Db 1869 AAAAGGATATTTATA 1883

RESULT 6
US-09-728-721-1
; Sequence 1, Application US/09728721
; Patent No. US20020061845A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/728,721
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/340,620

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; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-09-728-721-1

Query Match      43.8%; Score 731.8; DB 9; Length 1931;
Best Local Similarity 99.7%; Pred. No. 1.9e-143;
Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 331 ACAGTTACAGAGTGTTCAGAGTCCATTCACCTATGTGACAAAGAGAAATGGAATTATC 390
Db 1149 AAAGTTACAGAGTGTTCAGAGTCCATTCACCTATGTGACAAAGAGAAATGGAATTATC 1208

QY 391 TCTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCA 450
Db 1209 TCTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCA 1268

QY 451 TGAATAATAGTGTTCCTGAAATCTCAAGTCCCTGCCAGTCTCTCAAGACAAATGATTT 510
Db 1269 TGAATAATAGTGTTCCTGAAATCTCAAGTCCCTGCCAGTCTCTCAAGACAAATGATTT 1328

QY 511 TTTATCTAGAAAGCTCAAGACTGTATTTATGAAGTGCATCACTGTCTGGAATCA 570
Db 1329 TTTATCTAGAAAGCTCAAGACTGTATTTATGAAGTGCATCACTGTCTGGAATCA 1388

QY 571 CAGTTGGATAGCACCATTCTGGATCTCAAGGGGTGCAATCTGTGATCAAGACCAAC 630
Db 1389 CAGTTGGATAGCACCATTCTGGATCTCAAGGGGTGCAATCTGTGATCAAGACCAAC 1448

QY 631 TCCATGCTCTTCAGCAATATAATCACTCTCAACTGAGGAACTCAGAACTGCTGCA 690
Db 1449 TCCATGCTCTTCAGCAATATAATCACTCTCAACTGAGGAACTCAGAACTGCTGCA 1508

QY 691 GCCTGTATAGCCAGAGTGGATCCAGAGCAAGAGGAGACATTTGTGAACCAATGAC 750
Db 1509 GCCTGTATAGCCAGAGTGGATCCAGAGCAAGAGGAGACATTTGTGAACCAATGAC 1568

QY 751 AGAAGCTGCTTAAACGTCGTAGATGCCCTTCTGTCAGGAGCTTCATCATGAAGA 810
Db 1569 AGAAGCTGCTTAAACGTCGTAGATGCCCTTCTGTCAGGAGCTTCATCATGAAGA 1628

QY 811 GGAATTAAGTGTGTAGTACCAAGCTCAAGAGCTCAAGAGTCAAGCAATTAAGT 870
Db 1629 GGAATTAAGTGTGTAGTACCAAGCTCAAGAGCTCAAGAGTCAAGCAATTAAGT 1688

QY 871 CACTACTGACATCAAGAGGAGAAATTTGCAAGTTATAGTACAAAAATTTGAAGATAA 930
Db 1689 CACTACTGACATCAAGAGGAGAAATTTGCAAGTTATAGTACAAAAATTTGAAGATAA 1748

QY 931 CAACAAATAGGCTTTCAGCTTACCGGAAATCTTGTGTTTCTAGATCAACATCTTT 990
Db 1749 CAACAAATAGGCTTTCAGCTTACCGGAAATCTTGTGTTTCTAGATCAACATCTTT 1808

QY 991 AAATTTACTTCAAAATAAAGACATGTAAGTACTGTTTTTCAAGAGAAATGTTTTCAT 1050
Db 1809 AAATTTACTTCAAAATAAAGACATGTAAGTACTGTTTTTCAAGAGAAATGTTTTCAT 1868

QY 1051 AAAAGGATATTATA 1065
Db 1869 AAAAGGATATTATA 1883
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RESULT 7
US-10-133-780-2
; Sequence 2, Application US/10133780
; Publication No. US20020123115A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
; DOMAIN POLYPEPTIDES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/133,780
; FILING DATE: 26-Apr-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/019,942
; FILING DATE: 06-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/068001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1931 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-133-780-2

Query Match      43.8%; Score 731.8; DB 13; Length 1931;
Best Local Similarity 99.7%; Pred. No. 1.9e-143;
Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 331 ACAGTTACAGAGTGTTCAGAGTCCATTCACCTATGTGACAAAGAGAAATGGAATTATC 390
Db 1149 AAAGTTACAGAGTGTTCAGAGTCCATTCACCTATGTGACAAAGAGAAATGGAATTATC 1208

QY 391 TCTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCA 450
Db 1209 TCTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCA 1268

QY 451 TGAATAATAGTGTTCCTGAAATCTCAAGTCCCTGCCAGTCTCTCAAGACAAATGATTT 510
Db 1269 TGAATAATAGTGTTCCTGAAATCTCAAGTCCCTGCCAGTCTCTCAAGACAAATGATTT 1328

QY 511 TTTATCTAGAAAGCTCAAGACTGTATTTATGAAGTGCATCACTGTCTGGAATCA 570
Db 1329 TTTATCTAGAAAGCTCAAGACTGTATTTATGAAGTGCATCACTGTCTGGAATCA 1388

QY 571 CAGTTGGATAGCACCATTCTGGATCTCAAGGGGTGCAATCTGTGATCAAGACCAAC 630
Db 1389 CAGTTGGATAGCACCATTCTGGATCTCAAGGGGTGCAATCTGTGATCAAGACCAAC 1448

QY 631 TCCATGCTCTTCAGCAATATAATCACTCTCAACTGAGGAACTCAGAACTGCTGCA 690
Db 1449 TCCATGCTCTTCAGCAATATAATCACTCTCAACTGAGGAACTCAGAACTGCTGCA 1508

QY 691 GCCTGTATAGCCAGAGTGGATCCAGAGCAAGAGGAGACATTTGTGAACCAATGAC 750
Db 1509 GCCTGTATAGCCAGAGTGGATCCAGAGCAAGAGGAGACATTTGTGAACCAATGAC 1568

QY 751 AGAAGCTGCTTAAACGTCGTAGATGCCCTTCTGTCAGGAGCTTCATCATGAAGA 810
Db 1569 AGAAGCTGCTTAAACGTCGTAGATGCCCTTCTGTCAGGAGCTTCATCATGAAGA 1628

QY 811 GGAATTAAGTGTGTAGTACCAAGCTCAAGAGCTCAAGAGTCAAGCAATTAAGT 870
Db 1629 GGAATTAAGTGTGTAGTACCAAGCTCAAGAGCTCAAGAGTCAAGCAATTAAGT 1688

QY 871 CACTACTGACATCAAGAGGAGAAATTTGCAAGTTATAGTACAAAAATTTGAAGATAA 930
Db 1689 CACTACTGACATCAAGAGGAGAAATTTGCAAGTTATAGTACAAAAATTTGAAGATAA 1748

QY 931 CAACAAATAGGCTTTCAGCTTACCGGAAATCTTGTGTTTCTAGATCAACATCTTT 990
Db 1749 CAACAAATAGGCTTTCAGCTTACCGGAAATCTTGTGTTTCTAGATCAACATCTTT 1808

QY 991 AAATTTACTTCAAAATAAAGACATGTAAGTACTGTTTTTCAAGAGAAATGTTTTCAT 1050
Db 1809 AAATTTACTTCAAAATAAAGACATGTAAGTACTGTTTTTCAAGAGAAATGTTTTCAT 1868

QY 1051 AAAAGGATATTATA 1065
Db 1869 AAAAGGATATTATA 1883
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Db 1449 TCATGCTCTTACGCAATAATAAATCCACTCTCAACTGCGAGGAACTCAGAACTGCTGCA 1508
Qy 691 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACTGAC 750
Db 1509 GCCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACTGAC 1568
Qy 751 AGAAGCCTGCTTAAACAGTCGCTAGATGCGCTTCTGTCAGGACCTTGATCATGAAAGA 810
Db 1569 AGAAGCCTGCTTAAACAGTCGCTAGATGCGCTTCTGTCAGGACCTTGATCATGAAAGA 1628
Qy 811 GGACTATGAACTTGTAGTACCAAGCTCAAGGACCTCAAAAGTCAAGACCTGCTGCA 870
Db 1629 GGACTATGAACTTGTAGTACCAAGCTCAAGGACCTCAAAAGTCAAGACCTGCTGCA 1688
Qy 871 CACTACTGACATCCAAAGGAGAAATTTGCAAAAGTTATAGTCAAAATTTGAAAGATAA 930
Db 1689 CACTACTGACATCCAAAGGAGAAATTTGCAAAAGTTATAGTCAAAATTTGAAAGATAA 1748
Qy 931 CAAACAAATGGGTCTTCAGCCTTACCAGGAAATCTGTTGGTTCTAGATCAACATCTTT 990
Db 1749 CAAACAAATGGGTCTTCAGCCTTACCAGGAAATCTGTTGGTTCTAGATCAACATCTTT 1808
Qy 991 AAATTTACTTCAAAATAAAGCATGTAAGTGACTGTTTTCAGAGAAATGTTTTCAT 1050
Db 1809 AAATTTACTTCAAAATAAAGCATGTAAGTGACTGTTTTCAGAGAAATGTTTTCAT 1868
Qy 1051 AAAAGGATATTTATA 1065
Db 1869 AAAAGGATATTTATA 1883

RESULT 8

US-10-105-931-1
; Sequence 1, Application US/10105931
; Publication No. US20020150987A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/10/105,931
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-10-105-931-1

Query Match 43.8%; Score 731.8; DB 13; Length 1931;
Best Local Similarity 99.7%; Pred. No. 1.9e-143;
Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 331 ACAGTTACAGAGTGTTCAGTGCCATTACCTATGTGACAAAGAAAATGGAATTATC 390
Db 1149 AAGTTACAGAGTGTTCAGTGCCATTACCTATGTGACAAAGAAAATGGAATTATC 1208
Qy 391 TCTGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCTCTCAGTCCA 450
Db 1209 TCTGAACATACCTGTAAATCATGGTCCCAAGAGGAATCATGTGGATCTCTCAGTCCA 1268
Qy 451 TGAATATAGTGTCTCTCCTCAAGTTCAAGGTCCTGCCAGCTCCTCAAGACATGATTT 510
Db 1269 TGAATATAGTGTCTCTCCTCAAGTTCAAGGTCCTGCCAGCTCCTCAAGACATGATTT 1328

Qy 511 TTTATCTAGAAAGCTCAAGACTGTTATTTTATGAGCTGCATCACTGCTCTGGAATCA 570
Db 1329 TTTATCTAGAAAGCTCAAGACTGTTATTTTATGAGCTGCATCACTGCTCTGGAATCA 1388
Qy 571 CAGTTGGGATAGACCACTTTCTGGATCTCAAAGGGCTGCATTTCTGTGATCACAAGACCAC 630
Db 1389 CAGTTGGGATAGACCACTTTCTGGATCTCAAAGGGCTGCATTTCTGTGATCACAAGACCAC 1448
Qy 631 TCCATGCTCTTCCAGCAATAATAAATCACTCTCAACTGCGAGGAACTCAGAACGCTCTGCA 690
Db 1449 TCCATGCTCTTCCAGCAATAATAAATCACTCTCAACTGCGAGGAACTCAGAACGCTCTGCA 1508
Qy 691 GCCTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACTGAC 750
Db 1509 GCCTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACTGAC 1568
Qy 751 AGAAGCCTGCTTACCAGTCTAGATGCGCTTCTGTCAGGACCTTGATCATGAAAGA 810
Db 1569 AGAAGCCTGCTTACCAGTCTAGATGCGCTTCTGTCAGGACCTTGATCATGAAAGA 1628
Qy 811 GGACTATGAACTTGTAGTACCAAGCTCAAGGACCTCAAAAGTCAAGACCTTACTAGA 870
Db 1629 GGACTATGAACTTGTAGTACCAAGCTCAAGGACCTCAAAAGTCAAGACCTTACTAGA 1688
Qy 871 CACTACTGACATCCAAAGGAGAAATTTGCAAAAGTTATAGTCAAAATTTGAAAGATAA 930
Db 1689 CACTACTGACATCCAAAGGAGAAATTTGCAAAAGTTATAGTCAAAATTTGAAAGATAA 1748
Qy 931 CAAACAAATGGGTCTTCAGCCTTACCAGGAAATCTGTTGGTTCTAGATCAACATCTTT 990
Db 1749 CAAACAAATGGGTCTTCAGCCTTACCAGGAAATCTGTTGGTTCTAGATCAACATCTTT 1808
Qy 991 AAATTTACTTCAAAATAAAGCATGTAAGTGACTGTTTTCAGAGAAATGTTTTCAT 1050
Db 1809 AAATTTACTTCAAAATAAAGCATGTAAGTGACTGTTTTCAGAGAAATGTTTTCAT 1868
Qy 1051 AAAAGGATATTTATA 1065
Db 1869 AAAAGGATATTTATA 1883

RESULT 9

US-10-118-984-1
; Sequence 1, Application US/10118984
; Publication No. US20020197693A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/10/118,984
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-10-118-984-1

Query Match 43.8%; Score 731.8; DB 13; Length 1931;
Best Local Similarity 99.7%; Pred. No. 1.9e-143;

Matches 733; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 331 ACAGTTACAGAGTGTTCAGAGTGCATTCACCTATGTGACAAAGAAATGGAATTATC 390
Db 1149 AAGTTACAGAGTGTTCAGAGTGCATTCACCTATGTGACAAAGAAATGGAATTATC 1208
QY 391 TCTGAACATACCTGTAAATCATGTGTCACAGAGAAATCATGTGATCCTCTCAGCTCCA 450
Db 1209 TCTGAACATACCTGTAAATCATGTGTCACAGAGAAATCATGTGATCCTCTCAGCTCCA 1268
QY 451 TCAAAATAGTGTTCCTCGAACTTCAAGGTCCCTGCGAGCTCCTCAAGACAATGATTT 510
Db 1269 TCAAAATAGTGTTCCTCGAACTTCAAGGTCCCTGCGAGCTCCTCAAGACAATGATTT 1328
QY 511 TTTATCTAGAAAAGCTCAAGACTGTATTTATTAAGTGTGCATCATGTGCTGGAATCA 570
Db 1329 TTTATCTAGAAAAGCTCAAGACTGTATTTATTAAGTGTGCATCATGTGCTGGAATCA 1388
QY 571 CAGTTGGGATAGCACCATTTCTGGAATCTCAAGGGCTGCATTTCTGTGATCAAGACCAC 630
Db 1389 CAGTTGGGATAGCACCATTTCTGGAATCTCAAGGGCTGCATTTCTGTGATCAAGACCAC 1448
QY 631 TCCATGCTCTTCAAGCAATTAATCCACTCTCAACTGCAGGAACTCAGAACTGCTGCA 690
Db 1449 TCCATGCTCTTCAAGCAATTAATCCACTCTCAACTGCAGGAACTCAGAACTGCTGCA 1508
QY 691 GCCTGTATAGCCAGCAGTGGATCCAGAGAAAGGGAAGACATTTGGAACCAATGAC 750
Db 1509 GCCTGTATAGCCAGCAGTGGATCCAGAGAAAGGGAAGACATTTGGAACCAATGAC 1568
QY 751 AGAAGCTGCTTACCACTGCTAGATCCCTTCTGTCAGGGACTTGTATCAATGATCA 810
Db 1569 AGAAGCTGCTTACCACTGCTAGATCCCTTCTGTCAGGGACTTGTATCAATGATCA 1628
QY 811 GGACTATGAACCTTGTAGTACCAAGCCTCAAGGACTCAAGGACTTGTATCAATGATCA 870
Db 1629 GGACTATGAACCTTGTAGTACCAAGCCTCAAGGACTCAAGGACTTGTATCAATGATCA 1688
QY 871 CACTACTGATCCAAAGGAGAGAAATTCGCAAGTATAGTACAAATTTGAAGATAA 930
Db 1689 CACTACTGATCCAAAGGAGAGAAATTCGCAAGTATAGTACAAATTTGAAGATAA 1748
QY 931 CAAACAAATGGGTCTTACGCTTACCGGAAATACCTTGTGTTCTAGATCAACCTTT 990
Db 1749 CAAACAAATGGGTCTTACGCTTACCGGAAATACCTTGTGTTCTAGATCAACCTTT 1808
QY 991 AAATTTACTTCAAAATAAAGCATGTAAGTGAATGCTGTTTTCAGAGAAATGTTTCAT 1050
Db 1809 AAATTTACTTCAAAATAAAGCATGTAAGTGAATGCTGTTTTCAGAGAAATGTTTCAT 1868
QY 1051 AAAGGATATTTATA 1065
Db 1869 AAAGGATATTTATA 1883

RESULT 10
US-10-295-981-1
; Sequence 1, Application US/10295981
; Publication No. US20030120055A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/10/295,981
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-10-295-981-1

Query Match 43.8%; Score 731.8; DB 15; Length 1931;
Best Local Similarity 99.7%; Pred. No. 1.9e-143; Indels 0; Gaps 0;
Matches 733; Conservative 0; Mismatches 2;
QY 331 ACAGTTACAGAGTGTTCAGAGTGCATTCACCTATGTGACAAAGAAATGGAATTATC 390
Db 1149 AAGTTACAGAGTGTTCAGAGTGCATTCACCTATGTGACAAAGAAATGGAATTATC 1208
QY 391 TCTGAACATACCTGTAAATCATGTGTCACAGAGAAATCATGTGATCCTCTCAGCTCCA 450
Db 1209 TCTGAACATACCTGTAAATCATGTGTCACAGAGAAATCATGTGATCCTCTCAGCTCCA 1268
QY 451 TGAATAATAGTGTTCCTCTGAACTTCAAGGTCCCTGCGAGCTCCTCAAGACAATGATTT 510
Db 1269 TGAATAATAGTGTTCCTCTGAACTTCAAGGTCCCTGCGAGCTCCTCAAGACAATGATTT 1328
QY 511 TTTATCTAGAAAAGCTCAAGACTGTATTTATTAAGTGTGCATCATGTGCTGGAATCA 570
Db 1329 TTTATCTAGAAAAGCTCAAGACTGTATTTATTAAGTGTGCATCATGTGCTGGAATCA 1388
QY 571 CAGTTGGGATAGCACCATTTCTGGAATCTCAAGGGCTGCATTTCTGTGATCAAGACCAC 630
Db 1389 CAGTTGGGATAGCACCATTTCTGGAATCTCAAGGGCTGCATTTCTGTGATCAAGACCAC 1448
QY 631 TCCATGCTCTTCAAGCAATTAATCCACTCTCAACTGCAGGAACTCAGAACTGCTGCA 690
Db 1449 TCCATGCTCTTCAAGCAATTAATCCACTCTCAACTGCAGGAACTCAGAACTGCTGCA 1508
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QY 811 GGACTATGAACCTTGTAGTACCAAGCCTCAAGGACTCAAGGACTTGTATCAATGATCA 870
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QY 871 CACTACTGATCCAAAGGAGAGAAATTCGCAAGTATAGTACAAATTTGAAGATAA 930
Db 1689 CACTACTGATCCAAAGGAGAGAAATTCGCAAGTATAGTACAAATTTGAAGATAA 1748
QY 931 CAAACAAATGGGTCTTACGCTTACCGGAAATACCTTGTGTTCTAGATCAACCTTT 990
Db 1749 CAAACAAATGGGTCTTACGCTTACCGGAAATACCTTGTGTTCTAGATCAACCTTT 1808
QY 991 AAATTTACTTCAAAATAAAGCATGTAAGTGAATGCTGTTTTCAGAGAAATGTTTCAT 1050
Db 1809 AAATTTACTTCAAAATAAAGCATGTAAGTGAATGCTGTTTTCAGAGAAATGTTTCAT 1868
QY 1051 AAAGGATATTTATA 1065
Db 1869 AAAGGATATTTATA 1883
RESULT 11
US-10-641-684
; Sequence 684, Application US/10641643

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/ Publication No. US20040077003A1
/ GENERAL INFORMATION:
/ APPLICANT: Cocks, Benjamin G.
/ Suan G. Stuart
/ Jeffrey J. Seilhamer
/ TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
/ GENE EXPRESSION
/ NUMBER OF SEQUENCES: 1508
/ CORRESPONDENCE ADDRESS:
/ ADDRESSES: INCYTE PHARMACEUTICALS, INC.
/ STREET: 3174 PORTER DRIVE
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/641,643
/ FILING DATE: 14-Aug-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: <Unknown>
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Zeller, Karen J.
/ REGISTRATION NUMBER: 37,071
/ REFERENCE/DOCKET NUMBER: PA-0001 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 855-0555
/ TELEFAX: (650) 845-4166
/ INFORMATION FOR SEQ ID NO: 684:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1060 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: MPMGN0703
/ CLONE: 445186
/ SEQUENCE DESCRIPTION: SEQ ID NO: 684 :
US-10-641-643-684

Query Match 41.7%; Score 695.4; DB 16; Length 1060;
Best Local Similarity 99.7%; Pred. No. 6.4e-136;
Matches 707; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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QY 391 TCTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGTCCA 450
DB 412 TCTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGTCCA 471
QY 451 TGAATAAATA-GTGGTTCCTGAAACTTCAAGTCCCTGCGAGCTCTCAAGACAATGATT 509
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DB 592 ACAGTTGGGATAGCACCATTCTGGATCTCAAGGGCTGCATTCTGTGATCAAGACCA 651
QY 630 CTCATGCTCTTCAGCAATAAATAATCCACTCTCAACCTCAGAGAACTCAGAACGCTGTC 689
DB 652 CTCATGCTCTTCAGCAATAAATAATCCACTCTCAACCTCAGAGAACTCAGAACGCTGTC 711

RESULT 12
US-10-172-118-957
/ Sequence 957, Application US/10172118
/ Publication No. US20030224374A1
/ GENERAL INFORMATION:
/ APPLICANT: Dai, Hongyue
/ APPLICANT: He, Yudong
/ APPLICANT: Linsley, Peter
/ APPLICANT: Mao, Mao
/ APPLICANT: Roberts, Chris
/ APPLICANT: Van 't Veer, Laura
/ APPLICANT: Van de Vijver, Marc
/ APPLICANT: Bernards, Rene
/ TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
/ FILE REFERENCE: 9301-175-999
/ CURRENT APPLICATION NUMBER: US/10/172,118
/ CURRENT FILING DATE: 2002-06-14
/ PRIOR APPLICATION NUMBER: 60/380,770
/ PRIOR FILING DATE: 2002-05-14
/ NUMBER OF SEQ ID NOS: 2699
/ SEQ ID NO 957
/ LENGTH: 1623
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ PUBLICATION INFORMATION:
/ DATABASE ACCESSION NUMBER: NM 003821
/ DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-957

Query Match 41.0%; Score 684.8; DB 15; Length 1623;
Best Local Similarity 99.7%; Pred. No. 1.3e-133;
Matches 686; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 331 ACAGTTACAGAGTGTTCAGGTGCCATTCCACCTATGTGACAGAGAAATGGAATTATC 390
DB 936 AAGTTTACAGAGTGTTCAGGTGCCATTCCACCTATGTGACAGAGAAATGGAATTATC 995
QY 391 TCTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGTCCA 450
DB 996 TCTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGTCCA 1055
QY 451 TGAATAAATAGTGGTTCCTGAAACTTCAAGTCCCTGCCAGCTCTCTCAAGACAATGATT 510
DB 1056 TGAATAAATAGTGGTTCCTGAAACTTCAAGTCCCTGCCAGCTCTCTCAAGACAATGATT 1115
QY 511 TTTTATCTAGAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGCTCTGGAATCA 570
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Db 1596 AAATTTACTTCAAAATAAAGCATGTAA 1623

RESULT 13

US-10-342-887-957
; Sequence 957, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 957
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-957

Query Match 41.0%; Score 684.8; DB 16; Length 1623;

Best Local Similarity 99.7%; Pred. No. 1.3e-133;

Matches 686; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 331 ACAGTTACAGATGTTTCAAGTGCCATTCACCTATGTGACAAGAGAAATGGAATTATC 390
Db 936 AAGATTACAGATGTTTCAAGTGCCATTCACCTATGTGACAAGAGAAATGGAATTATC 995

Qy 391 TCTGAACATACCTGTAAATCATGTGTCACAAGAGGAATCATGTGGATCCTCTCAGCTCCA 450
Db 996 TCTGAACATACCTGTAAATCATGTGTCACAAGAGGAATCATGTGGATCCTCTCAGCTCCA 1055
Qy 451 TGAATAATAGTGGTCTCTCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTT 510
Db 1056 TGAATAATAGTGGTCTCTCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTT 1115
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Db 1116 TTTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCCTGGAAATCA 1175
Qy 571 CAGTTGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCAC 630
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Db 1596 AAATTTACTTCAAAATAAAGCATGTAA 1623

RESULT 14

US-09-728-721-3
; Sequence 3, Application US/09728721
; Patent No. US20020061845A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/728,721
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-728-721-3

Query Match 40.9%; Score 681.8; DB 9; Length 1620;
Best Local Similarity 99.7%; Pred. No. 5.6e-133;

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(without alignments)
5232.035 Million cell updates/sec

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Perfect score: 2880
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Searched: 1608061 seqs, 361289386 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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No.	Score	Match	Length	DB	ID	Description
1	1206	41.9	232	9	US-09-771-161A-93	Sequence 93, Appl
2	1182	41.0	540	9	US-09-771-161A-184	Sequence 184, App
3	1182	41.0	540	9	US-09-862-027-28	Sequence 28, Appl
4	1182	41.0	540	10	US-09-981-397A-14	Sequence 14, Appl
5	1182	41.0	540	17	US-10-825-282-36	Sequence 36, Appl
6	1182	41.0	544	9	US-09-925-301-1015	Sequence 1015, Ap
7	1176	40.8	540	9	US-09-748-537-1	Sequence 1, Appli
8	1176	40.8	540	9	US-09-728-721-2	Sequence 2, Appli
9	1176	40.8	540	13	US-10-133-780-1	Sequence 1, Appli
10	1176	40.8	540	13	US-10-105-931-2	Sequence 2, Appli
11	1176	40.8	540	13	US-10-118-984-2	Sequence 2, Appli
12	1176	40.8	540	14	US-10-295-981-2	Sequence 2, Appli
13	632	21.9	131	9	US-09-728-721-5	Sequence 5, Appli
14	632	21.9	131	13	US-10-105-931-5	Sequence 5, Appli
15	632	21.9	131	13	US-10-118-984-5	Sequence 5, Appli
16	632	21.9	131	14	US-10-295-981-5	Sequence 5, Appli
17	544	18.9	109	9	US-09-728-721-6	Sequence 6, Appli
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22	461	16.0	92	13	US-10-002-974-21	Sequence 21, Appl
23	461	16.0	92	14	US-10-314-506-21	Sequence 21, Appl
24	451	15.7	90	9	US-09-841-879B-10	Sequence 10, Appl
25	451	15.7	90	16	US-10-756-097-10	Sequence 10, Appl
26	447	15.5	89	9	US-09-931-071-11	Sequence 11, Appl
27	149.5	5.2	109	9	US-09-728-721-71	Sequence 71, Appl
28	149.5	5.2	109	14	US-10-295-981-71	Sequence 71, Appl
29	143.5	5.0	95	9	US-09-841-879B-12	Sequence 12, Appl
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33	122.5	4.3	164	14	US-10-295-981-41	Sequence 41, Appl
34	122.5	4.3	249	9	US-09-728-721-39	Sequence 39, Appl
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41	122.5	4.3	953	14	US-10-013-477-12	Sequence 12, Appl
42	122.5	4.3	953	14	US-10-295-981-8	Sequence 8, Appli
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44	122.5	4.3	953	14	US-10-183-770-4	Sequence 4, Appli
45	119	4.1	100	9	US-09-728-721-10	Sequence 10, Appl

ALIGNMENTS

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RESULT 1
US-09-771-161A-93
; Sequence 93, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 93
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-771-161A-93

Alignment Scores:
Pred. No.: 4,68e-118 Length: 232
Score: 1206.00 Matches: 232
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 41.88% Indels: 0
DB: 9 Gaps: 0

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QY 800 ATCATGAAGAGACTATGAACCTGTGTAGTACCAAGCTTACAGGACCTCAAAAGTCAGA 859
Db 161 IleMetLysGluAspTyrGluLeuValSerThrLysProThrArgThrSerLysValArg 180
QY 860 CAATTACTAGACTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAA 919
Db 181 GlnLeuLeuAspThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLys 200
QY 920 TTGAAGATACAAACAAATGGTCTTTCAGCCCTTACCGGAATATCTGTGGTTTCTAGA 979
Db 201 LeuLysAspAsnLysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArg 220
QY 980 TCACCATCTTAAATTTACTTCAAAATAAAGCATG 1015
Db 221 SerProSerLeuAsnLeuLeuGlnAsnLysSerMet 232
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RESULT 2

US-09-771-161A-184
; Sequence 184, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776

; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 184
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-184

Alignment Scores:

Pred. No.: 2,08e-115 Length: 540
Score: 1182.00 Matches: 227
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.56% Mismatches: 0
Query Match: 41.04% Indels: 0
DB: 9 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-771-161A-184 (1-540)

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QY 332 CAGTTACAGAGTGTTCAGTGCATTCACCTATGTGACAGAGAAATGGAATATCT 391
Db 313 LysLeuGlnSerValSerSerAlaIleHisLeuCyAspLysLysMetGluLeuSer 332
QY 392 CTGAACATACCTGTAAATCATGTGTCACAGAGGAAATCATGTGGATCTCTCAGCTCCAT 451
Db 333 LeuAsnIleProValAsnHisGlyProGlnGlnGluSerCysGlySerSerGlnLeuHis 352
QY 452 GAAATAGTGGTCTCTCTGAAACTTCAAGGTCCCTGCCAGCTCTCAAGACAAATGATTTT 511
Db 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372
QY 512 TTATCTGAAAGCTCAAGACTGTGTATTTTATGAAGCTGCATCATCTGCTGGAATCATC 571
Db 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392
QY 572 AGTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTCGTGTGATCACAAGACCCT 631
Db 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 412
QY 632 CCATCTCTTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGTCTGCAG 691
Db 413 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
QY 692 CTGTGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGAGACATTTGTGAACCAATGACA 751
Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452
QY 752 GAAGCTCCCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGCATCATGAAAGAG 811
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
QY 812 GACTATGAACCTTGTGTAGTACCAAGCTTCAAGGACCTCAAAAGTGCAGACAATTTACTAGAC 871
Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGACATCCAAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAC 931
Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AAACAAATGGGTCTTTCAGCCTTTACCGGAAATPACTTGTGGTTCTTAGATCACCATCTTTA 991
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532
QY 992 AATTTACTTCAAAATAAAGCATG 1015
Db 533 AsnLeuLeuGlnAsnLysSerMet 540
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RESULT 3

US-09-862-027-28
; Sequence 28, Application US/09862027
; Patent No. US20020142428A1

RESULT 4

US-09-981-397A-14
; Sequence 14, Application US/09981397A
; Publication No. US20030082519A1
; GENERAL INFORMATION:
; APPLICANT: Axxima Pharmaceuticals AG
; APPLICANT: Schubart, Daniel
; APPLICANT: Habenberger, Peter
; APPLICANT: Stein-Gerlach, Matthias
; APPLICANT: Bevec, Dorian
; TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their
; TITLE OF INVENTION: Inhibition
; FILE REFERENCE: AXM-004.1 US
; CURRENT APPLICATION NUMBER: US/09/981.397A
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/240,750
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-981-397A-14

Alignment Scores:
Pred. NO.: 2.08e-115 Length: 540
Score: 1182.00 Matches: 227
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.56% Mismatches: 0
Query Match: 41.04% Indels: 0
DB: 10 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-981-397A-14 (1-540)

Qy	332	CAGTTACAGAGTGTTTCAAGTGCCATTCACTTGTGACAGAGAAATGGAATTATCT	391
Db	313	LYSLEUDGINSERVALSERSERALAEHISLEUCYASPLYSLYSMETGLUUEUSER	332
Qy	392	CTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT	451
Db	333	LEUASNILEPROVALASNHISGLYPROGLNGLUISERCYSGLYSERSERGINTLEUHS	352
Qy	452	GAATAATAGTGGTTCTCTGAAACTTCAAGTCCCTGCCAGCTCCTCAAGACAAATGATTTT	511
Db	353	GLUASNISERGLYSERPROGLIUTHRSERARGSERLEUPROALAProGLINAspAsnAspPhe	372
Qy	512	TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGTCTGGAATACAC	571
Db	373	LEUSERARGYSLALAGINAspCYSTYRPhemetLysLEUHSISCYSPROGLYASNHS	392
Qy	572	AGTTGGGATAGCACCATTTCTGGATCTCAAAAGGCTGCATTTCTGTGATCACAAGACCCT	631
Db	393	SERTRPASPSETHRIIESERGLYSERGLNARGALALAPHECYASPHISLSTHRT	412
Qy	632	CCATGCTCTTCAGCAATAATAATCCACTCTCACTGAGGAAACTCAGAACGCTGCGAG	691
Db	413	PROCYSSERSERALAEHISASNPROLEUSERTHRALAGLIYASNISERGLUARGLEUGIN	432
Qy	692	CCTGGTATAGCCACGACGTGATCCAGAGCAAAAGGAGACATTGTGAACCCAAATGACA	751
Db	433	PROGLYLEALAGLINTPILSELISERLYSARGGLUASPLILEVALSNGLNMETTHR	452
Qy	752	GAAGCCCTCCCTAAACCAAGTCCTAGATGCCCTTCTGTCCAGGACTTCGATCATGAAAGAG	811
Db	453	GLUALACYSEULEASNGLINSERLEUASPALALEULEUSERARGASPLEULETLYSGLU	472
Qy	812	GACTATGAACCTGTGTAGTACCAAGCTACAGAGCACTCAAAGTCAGACCAATTACTAGAC	871
Db	473	ASPTYRGLULEUVALSERTHRLYSERPROTHRARGTHRSERLYSVALARGGLNLEULEUASP	492
Qy	872	ACTACTGACATCCCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAAGATAAC	931

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Db 493 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
Qy 932 AAACAAATGGTCTTCAGCCTTACCCGGAATACTTGTGGTTCTAGATCACCATCTTTA 991
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 532
Qy 992 AATTACTTCAAAATAAAGCATG 1015
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 5
US-10-825-282-36
; Sequence 36, Application US/10825282
; Publication No. US20040224389A1
; GENERAL INFORMATION:
; APPLICANT: 3921-1-1-1
; TITLE OF INVENTION: VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3921-1-1-1
; CURRENT APPLICATION NUMBER: US/10/825,282
; PRIOR FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/456,357
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: 60/134,416
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 09/087,195
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 08/378,507
; PRIOR FILING DATE: 1995-01-26
; PRIOR APPLICATION NUMBER: 08/250,478
; PRIOR FILING DATE: 1994-05-27
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-825-282-36

Alignment Scores:
Pred. No.: 2,08e-115 Length: 540
Score: 1182.00 Matches: 227
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.56% Mismatches: 0
Query Match: 41.04% Indels: 0
DB: 17 Gaps: 0

US-09-771-161A-2 (1-1669) x US-10-825-282-36 (1-540)
Qy 332 CAGTTACAGAGTGTTCAGTGCCTTACCTATGTGACAGAGAAATGGAATTATCT 391
Db 313 LysLeuGlnSerValSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332
Qy 392 CTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGCATCCTCTCAGCTCCAT 451
Db 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 352
Qy 452 GAAATAGTGGTCTCTCGAAATCTCAAGTCCCTGCAGCTCCTCAAGACAATGATTTT 511
Db 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372
Qy 512 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGTGCATCAGTCTCGGAAATCAC 571
Db 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392
Qy 572 AGTTGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTCTGTGATCAACAAGACCAT 631
Db 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 412
Qy 632 CCATGCTTTCAGCAATAATAATCCACTCTCACTGCAGAACTCAGAACGCTTCGAG 691
Db 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
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Qy 692 CCTGGTATAGCCCGACAGTGGATCCAGAGCAAAAGGGAAGACATTGTGAACCAATGACA 751
Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452
Qy 752 GAAGCCTGCCCTTAACCAAGTCGTAGATGCCCTTCTGTCCAGGGACTTGTATCATGAAAGAG 811
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
Qy 812 GACTATGAACCTTGTAGTACCAAGCCTTACAGGACCTCAAAAGTCAGACAATTTACTAGAC 871
Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
Qy 872 ACTACTGACATCCCAAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 931
Db 493 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
Qy 932 AAACAAATGGTCTTTCAGCCTTACCCGGAATACTTGTGGTTCTAGATCACCATCTTTA 991
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 532
Qy 992 AATTACTTCAAAATAAAGCATG 1015
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 6
US-09-925-301-1015
; Sequence 1015, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1015
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1015

Alignment Scores:
Pred. No.: 2,09e-115 Length: 544
Score: 1182.00 Matches: 227
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.56% Mismatches: 0
Query Match: 41.04% Indels: 0
DB: 9 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-925-301-1015 (1-544)
Qy 332 CAGTTACAGAGTGTTCAGTGCCTTACCTATGTGACAGAGAAATGGAATTATCT 391
Db 317 LysLeuGlnSerValSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 336
Qy 392 CTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGCATCCTCTCAGCTCCAT 451
Db 337 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 356
Qy 452 GAAATAGTGGTCTCTCGAAATCTCAAGTCCCTGCAGCTCCTCAAGACAATGATTTT 511
Db 357 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 376
Qy 512 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGTGCATCAGTCTCGGAAATCAC 571
Db 377 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 396
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QY 572 AGTTGGATAGCACCATTCTTGGATCTCAAGAGGCTGCAATCTCTGTGATCAAGACCACT 631
Db SerTpaSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 416
QY 632 CCATGCTCTTCAGCAATAAATCACTCTCACTGACGAGAACTCAGAACGCTCTGCAG 691
Db ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 436
QY 692 CCTGGTATAGCCAGCAGTGGATCCAGACAAAGGGAAGACATTTGAAACCAATGACA 751
Db ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 456
QY 752 GAAGCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGACCTGTGATCAAGAAAG 811
Db GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 476
QY 812 GACTATGACCTTGTAGTACCAAGCTTACCAAGACCTCAAAAGTCAGCAATTTACTAGAC 871
Db AspTyrGlnLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 496
QY 872 ACTACTGACATCAAGGAGAGAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 931
Db ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 516
QY 932 AAACAAATGGTCTTCAGCCTTACCCGGAATACTTGTGTGTTCTAGATCACCATCTTTA 991
Db LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 536
QY 992 AATTACTTCAAAATAAAAGCATG 1015
Db AsnLeuLeuGlnAsnLysSerMet 544

RESULT 7

US-09-748-537-1

; Sequence 1, Application US/09748537
; Patent No. US20020061833A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Chao, Moses V.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-316001
; CURRENT APPLICATION NUMBER: US/09/748,537
; PRIOR FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-748-537-1

Alignment Scores:
Pred. No.: 8 96e-115 Length: 540
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 40.83% Indels: 0
DB: 9 Gaps: 0

US-09-771-161A-2 (1-1669) x US-09-748-537-1 (1-540)

QY 332 CAGTTACAGAGTGTTCAGTGCCTTCACTATGTGACAAAGAAATGGAATATCT 391
Db LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332
QY 392 CTGAACATACCTGTAAATCATGTGTCACAGAGAAATCATGTGATCCTCTCAGTCCAT 451
Db LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 352

QY 452 GAAATAGTGGTCTCTCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT 511
Db GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372
QY 512 TTATCTAGAAAAGCTCAAGACTGTGTTATTTTATGAAGCTGCATCCTGCTGGAATCAC 571
Db LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392
QY 572 AGTTGGATAGCACCATTCTTGGATCTCAAGAGGCTGCAATCTCTGTGATCAAGACCACT 631
Db SerTpaSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 412
QY 632 CCATGCTCTTCAACCAATAAATCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAG 691
Db ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
QY 692 CCTGGTATAGCCAGCAGTGGATCCAGACAAAGGGAAGACATTTGTAACCAATGACA 751
Db ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452
QY 752 GAAGCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGACCTTGATCATGAAAGAG 811
Db GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
QY 812 GACTATGAACTTGTAGTACCAAGCTTACCAAGACCTCAAAAGTCAGCAATTTACTAGAC 871
Db AspTyrGlnLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGACATCAAGGAGAGAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 931
Db ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AAACAAATGGTCTTCAGCCTTACCCGGAATACTTGTGTGTTCTAGATCACCATCTTTA 991
Db LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532
QY 992 AATTACTTCAAAATAAAAGCATG 1015
Db AsnLeuLeuGlnAsnLysSerMet 540

RESULT 8

US-09-728-721-2

; Sequence 2, Application US/09728721
; Patent No. US20020061845A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/728,721
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-728-721-2

Alignment Scores:
Pred. No.: 8 96e-115 Length: 540
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 40.83% Indels: 0
DB: 9 Gaps: 0

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US-09-771-161A-2 (1-1669) x US-09-728-721-2 (1-540)
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QY 332 CAGTTACAGAGTGTTCAGTGCCATTCACTATGTCACAAGAAGAAATGGATTATCT 391
Db ::::|||||
QY 333 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332
QY 392 CTGAACATACTGTAATCATCGTCCACAAGAGGAATCATGTGGATCCTCTCACGCCAT 451
Db |||||ProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 352

QY 452 GAAAAATAGTGGTCTCCTGAAAATCTCAAGTCCCTGCAGCTCTCAAGAACATGATTIT 511
Db GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPhe 372

QY 512 TTATCTAGAAAAGCTCAAGACTGTTATTTTTATGAAGTGCATCATCTGTCCTGGAAATCAC 571
Db |||||LeuSerArgLysAlaGlnAspCysTyrrPheMetLysLeuHisCysProGlyAsnHis 392

QY 572 AGTTGGATAGCACCATTCTGGATCTCAAAGGCTCCCTGCAGCTCTCAAGAACATGATTIT 540
Db SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 412

QY 632 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACCTCAGAACGCTGCAG 691
Db ProCysSerSerAlaIleLeasnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432

QY 692 CCTGGTATAGCCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGTAACCAATGACA 751
Db |||||ProGlyIleAlaGlnInrPileGlnSerLysArgGluAspIleValAsnGlnMethr 452

QY 752 GAAGCTGCCTTAAACCAGTCCGTAGTAGTCCCTTCTGTCACAGGACTTCATCATGAAAG 811
Db GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472

QY 812 GACTATGAACCTTGTAGTACCAGGCTCAAGGACTCAAGGACTCAAGGACTCAAGGACT 871
Db AspTyrrGluLeuValSerThrLysPr-oThrArgThrSerLysValArgGlnLeuLeuAsp 492

QY 872 ACTACTGACATCCAAGGAGAAATTTGCAAGTATTATAGTACAAAATTTGAAAGATAAC 931
Db ThrThraspileGlnGlyGluPheAlalysValIleValGlnLysLeuLysAspAsn 512

QY 932 AAACAAATGGTCTTCAGCTWTACC CGGAAATCTGTGTTCTTCTAGATCACCATTCTTA 991
Db LysGlnMetGlyLeuGlnProTyrrProGluIleLeuValValSerArgSerProSerLeu 532

QY 992 AATTACTTCAAAATAAAGCATG 1015
Db AsnLeuLeuGlnAsnLysSerMet 540

RESULT 9
US-10-133-780-1
; Sequence 1, Application US/10133780
; Publication No. US20020123115A1
GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:


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Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532
QY 992 AATTACTTCAAAATAAAGCATG 1015
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 10
US-10-105-931-2
; Sequence 2, Application US/10105931
; Publication No. US20020150987A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/10/105,931
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/099,941
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-931-2

Alignment Scores:
Pred. No.: 8,96e-115 Length: 540
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservatives: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 40.83% Indels: 0
DB: 13 Gaps: 0

US-09-771-161A-2 (1-1669) x US-10-105-931-2 (1-540)
QY 332 CAGTTACAGAGTGTTCAGTGCATTCACCTATGTGACAGAGAAATGGAATTATCT 391
Db 313 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332
QY 392 CTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGCATCCTCTCAGCTCCAT 451
Db 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 352
QY 452 GAAATATAGTGGTCTCTCTGAAACTTCAAGTCCCTGCGAGCTCCTCAAGACATGATTTT 511
Db 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnApphe 372
QY 512 TTATCTAGAAAAGCTCAAGCTGTTATTTATGAAGCTGCATCAGTCTCGAATATCAT 571
Db 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392
QY 572 AGTTGGATAGCACCATTCTGATCTCAAGGCTGCATTCGTGATCAGAGACCAT 631
Db 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaPheCysAspHisLysThrIle 412
QY 632 CCATGCTCTTCAGCAATAATAATCCACTCTCAAGTCCGAGAACTCAGAACATGATTTT 691
Db 413 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
QY 692 CTGTGATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTAACCAATGACA 751
Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452
QY 752 GAAGCTGCTTAAACAGTCGTAGATGCCCTTCTGTCCAGGACACTGTATCATGAAGAG 811
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
QY 812 GACTATGAACCTTGTAGTACCAAGCCTTACAAGGACCTCAAAAGCTCAGAACTACTAGAC 871
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Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGACATCAAGGAGAAGATTTCGCAAGTTATAGTACAAAATTTGAAAGATAAC 931
Db 493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AAACAAATGGTCTTTCAGCCTTACCCGGAATACTTGTGTTCTAGATCACCATCTTTA 991
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532
QY 992 AATTACTTCAAAATAAAGCATG 1015
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

RESULT 11
US-10-118-984-2
; Sequence 2, Application US/10118984
; Publication No. US20020197693A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/10/118,984
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-02-05
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-02-05
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-06-17
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-02-06
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-118-984-2

Alignment Scores:
Pred. No.: 8,96e-115 Length: 540
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservatives: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 40.83% Indels: 0
DB: 13 Gaps: 0

US-09-771-161A-2 (1-1669) x US-10-118-984-2 (1-540)
QY 332 CAGTTACAGAGTGTTCAGTGCATTCACCTATGTGACAGAGAAATGGAATTATCT 391
Db 313 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332
QY 392 CTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGCATCCTCTCAGCTCCAT 451
Db 333 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 352
QY 452 GAAATATAGTGGTCTCTCTGAAACTTCAAGTCCCTGCGAGCTCCTCAAGACATGATTTT 511
Db 353 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnApphe 372
QY 512 TTATCTAGAAAAGCTCAAGCTGTTATTTATGAAGCTGCATCAGTCTCGAATATCAT 571
Db 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392
QY 572 AGTTGGATAGCACCATTCTGATCTCAAGGCTGCATTCGTGATCAGAGACCAT 631
Db 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaPheCysAspHisLysThrIle 412
QY 632 CCATGCTCTTCAGCAATAATAATCCACTCTCAAGTCCGAGAACTCAGAACCTCTGCGAG 691
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Db 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
QY 692 CTGGTATAGCCAGAGATCCAGAGCAAGGAAAGACATTTGTGAACCAATGACA 751
Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452
QY 752 GAAGCCTGGCTTAACAGTCGCTAGATGCCCTCTCTCCAGGACTTGATCATGAAGAG 811
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
QY 812 GACTATGAACTTGTAGTACCAAGCCTACAAGGACCTCAAAAGCTCAGACAATTTACTAGAC 871
Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGACATCAAGAGAGAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 931
Db 493 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AACCAATGGCTTCAGCCTTACCCGGAATACTTGTGTCTAGATCACCATCTTTA 991
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532
QY 992 AATTACTTCAAAATAAAGCATG 1015
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US-10-295-981-2
; Sequence 2, Application US/10295981
; Publication No. US20030120055A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/10/295,981
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US/09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US/09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US/09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-981-2

Alignment Scores:
Pred. No.: 8,96e-115 Length: 540
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 40.83% Indels: 0
DB: 14 Gaps: 0

US-09-771-161A-2 (1-1669) x US-10-295-981-2 (1-540)

QY 332 CAGTTACAGAGTGTTCCTGATGCAATTCACCTATGACAAAGAAATGAAATATCT 391
Db 313 LysLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 332
QY 392 CTGAACATACCTGTAAATCATGTCACAGAGGAATCATGTGGATCTCTCAGCTCCAT 451
Db 333 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerGlnLeuHis 352

QY 452 GAABAATAGTGGTTCCTCGAARACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTT 511
Db 353 GluAsnSerGlySerProGlnThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 372
QY 512 TTATCTAGAAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCTCTGGAATCAC 571
Db 373 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 392
QY 572 AGTTGGGATAGACCACTTTCTGGATCTCAAAGGGTGCATTTCTGTGATCACAAGACCCT 631
Db 393 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrIle 412
QY 632 CCATCTCTTCCAGCAATAAATCACTCTCAACTGCAGGAACTCAGAACGTCTGCAG 691
Db 413 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
QY 692 CTGTGTATAGCCCAAGCAGTGGATCCAGAGCAAGGAAAGACATTTGTGAACCAATGACA 751
Db 433 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 452
QY 752 GAAGCCTGGCTTAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAG 811
Db 453 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 472
QY 812 GACTATGAACTTGTAGTACCAAGCCTACAAGGACCTCAAAAGTTATAGTACAAAATTTGAAAGATAAC 871
Db 473 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 492
QY 872 ACTACTGACATCAAGAGAGAATTTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 931
Db 493 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 512
QY 932 AAACAAATGGGTTCCTCAGCCTTACCCGGAATACTTGTGTCTAGATCACCATCTTTA 991
Db 513 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 532
QY 992 AATTACTTCAAAATAAAGCATG 1015
Db 533 AsnLeuLeuGlnAsnLysSerMet 540

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US-09-728-721-5
; Sequence 5, Application US/09728721
; Patent No. US20020061845A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/728,721
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US/09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US/09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US/09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-728-721-5

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Score: 632.00 Matches: 117
Percent Similarity: 99.16% Conservative: 1
Best Local Similarity: 98.32% Mismatches: 1
Query Match: 21.94% Indels: 0
DB: 9 Gaps: 0

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DB 13 LysLeuGlnSerValSerSerAlaHisLeuCysAspLysMetGluLeuSer 32
QY 392 CTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCAT 451
DB 33 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 52
QY 452 GAAAATAGTGTCTCTCGTAACCTCAAGGTCCTCCAGCTCCTCAAGACAAATGATTTT 511
DB 53 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnApphe 72
QY 512 TTATCTAGAAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACCTCTCTGGAATACAC 571
DB 73 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 92
QY 572 AGTTGGGATAGCACCATTTCTGGATCTCAAAGGCTGCATTTCTGTGATCATCAGAACCT 688
DB 93 SerTrpAspSerThrIleSerGlySerGlnArgAlaPheCysAspHisLysThrIle 112
QY 632 CCATGCTCTTCAGCAATAATAATCCAATCTCAACTCGAGGAACCTCAGAACGCTCTG 688
DB 113 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeu 131
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US-10-118-984-5
; Sequence 5, Application US/10118984
; Publication No. US20020197693A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/10/118,984
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/207,359
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/099,041
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/019,942
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-118-984-5
Alignment Scores:
Pred. No.: 1,66e-57 Length: 131
Score: 632.00 Matches: 117
Percent Similarity: 99.16% Conservative: 1
Best Local Similarity: 98.32% Mismatches: 1
Query Match: 21.94% Indels: 0
DB: 13 Gaps: 0
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QY 332 CAGTTACAGAGTGTTCCTCAAGTGCCATTCACTATGTCACAAGAAGAAATGAATATCT 391
DB 13 LysLeuGlnSerValSerSerAlaHisLeuCysAspLysMetGluLeuSer 32
QY 392 CTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCAT 451
DB 33 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 52
QY 452 GAAAATAGTGTCTCTCGTAACCTCAAGGTCCTCCAGCTCCTCAAGACAAATGATTTT 511
DB 53 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnApphe 72
QY 512 TTATCTAGAAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACCTCTCTGGAATACAC 571
DB 73 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 92
QY 572 AGTTGGGATAGCACCATTTCTGGATCTCAAAGGCTGCATTTCTGTGATCATCAGAACCT 688
DB 93 SerTrpAspSerThrIleSerGlySerGlnArgAlaPheCysAspHisLysThrIle 112
QY 632 CCATGCTCTTCAGCAATAATAATCCAATCTCAACTCGAGGAACCTCAGAACGCTCTG 688
DB 113 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeu 131

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US-09-771-161A-2 (1-1669) x US-09-728-721-5 (1-131)
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DB 13 LysLeuGlnSerValSerSerAlaHisLeuCysAspLysMetGluLeuSer 32
QY 392 CTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCAT 451
DB 33 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 52
QY 452 GAAAATAGTGTCTCTCGTAACCTCAAGGTCCTCCAGCTCCTCAAGACAAATGATTTT 511
DB 53 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnApphe 72
QY 512 TTATCTAGAAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACCTCTCTGGAATACAC 571
DB 73 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 92
QY 572 AGTTGGGATAGCACCATTTCTGGATCTCAAAGGCTGCATTTCTGTGATCATCAGAACCT 688
DB 93 SerTrpAspSerThrIleSerGlySerGlnArgAlaPheCysAspHisLysThrIle 112
QY 632 CCATGCTCTTCAGCAATAATAATCCAATCTCAACTCGAGGAACCTCAGAACGCTCTG 688
DB 113 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeu 131
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; Sequence 5, Application US/10105931
; Publication No. US20020150987A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/10/105,931
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-931-5
Alignment Scores:
Pred. No.: 1,66e-57 Length: 131
Score: 632.00 Matches: 117
Percent Similarity: 99.16% Conservative: 1
Best Local Similarity: 98.32% Mismatches: 1
Query Match: 21.94% Indels: 0
DB: 13 Gaps: 0
US-09-771-161A-2 (1-1669) x US-10-105-931-5 (1-131)
QY 332 CAGTTACAGAGTGTTCCTCAAGTGCCATTCACTATGTCACAAGAAGAAATGAATATCT 391
DB 13 LysLeuGlnSerValSerSerAlaHisLeuCysAspLysMetGluLeuSer 32
QY 392 CTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCAT 451
DB 33 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerGlnLeuHis 52
QY 452 GAAAATAGTGTCTCTCGTAACCTCAAGGTCCTCCAGCTCCTCAAGACAAATGATTTT 511
DB 53 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnApphe 72
QY 512 TTATCTAGAAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACCTCTCTGGAATACAC 571

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Tue Feb 1 09:12:07 2005

us-09-771-161a-2.rapb

Page 10

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Job time : 243.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 28, 2005, 12:37:13 ; Search time 39 Seconds
(without alignments)
394.507 Million cell updates/sec

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Perfect score: 1206
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Scoring table: BLOSUM62
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Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	1182	98.0 531 3	US-09-069-023-1 Sequence 1, Appli
5	1182	98.0 540 3	US-09-069-023-27 Sequence 27, Appli
6	1182	98.0 540 4	US-09-345-473B-28 Sequence 28, Appli
7	1176	97.5 540 3	US-09-019-942-1 Sequence 1, Appli
8	1176	97.5 540 3	US-09-099-041A-2 Sequence 2, Appli
9	1176	97.5 540 3	US-09-245-281-2 Sequence 2, Appli
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19	632	52.4 131 4	US-09-340-620A-5 Sequence 5, Appli
20	632	52.4 131 4	US-09-865-364-5 Sequence 5, Appli
21	548	45.4 110 4	US-09-207-359B-6 Sequence 6, Appli
22	548	45.4 110 4	US-09-865-364-6 Sequence 6, Appli
23	544	45.1 109 3	US-09-099-041A-6 Sequence 6, Appli
24	544	45.1 109 3	US-09-245-281-6 Sequence 6, Appli
25	544	45.1 109 4	US-09-340-620A-6 Sequence 6, Appli
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RESULT 1

US-09-069-023-5

; Sequence 5, Application US/09069023A

; Patent No. 6348573

GENERAL INFORMATION:

; APPLICANT: Nunez, Gabriel

; APPLICANT: Inohara, Naohiro

; APPLICANT: Koseki, Takeyoshi

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS

; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS

; FILE REFERENCE: UM-03333

; CURRENT APPLICATION NUMBER: US/09/069,023A

; CURRENT FILING DATE: 1998-04-27

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5

; LENGTH: 284

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-069-023-5

Query Match		98.0%	Score 1182;	DB 3;	Length 284;
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Db	177	PGIAQOWIQSKREDIVNQMTACLQSLDALLSRDLIMKEDYELVSTKTRTSKVRQLLD	236		
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US-09-069-023-4

; Sequence 4, Application US/09069023A

; Patent No. 6348573

GENERAL INFORMATION:

; APPLICANT: Nunez, Gabriel

; APPLICANT: Inohara, Naohiro

; APPLICANT: Koseki, Takeyoshi

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; FILE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-0333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-4

Query Match 98.0%; Score 1182; DB 3; Length 478;
Best Local Similarity 99.6%; Pred. No. 5.2e-125;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 5 QLOSVSSAIHLCDKKKMWELSLNIPVNHGPOEESCGSSQLHENS GSPETSRSLPAPQDNDF 64
Db 251 KLOSVSSAIHLCDKKKMWELSLNIPVNHGPOEESCGSSQLHENS GSPETSRSLPAPQDNDF 310
QY 65 LSRKAQDCYFMKLHHCPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124
Db 311 LSRKAQDCYFMKLHHCPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 370
QY 125 PGIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
Db 371 PGIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 430
QY 185 TTDIOGEEFAKVIQVKLKNQKMGLOQYPPEILVVSRSPLNLLQNKSM 232
Db 431 TTDIOGEEFAKVIQVKLKNQKMGLOQYPPEILVVSRSPLNLLQNKSM 478

RESULT 3
US-09-069-023-3
; Sequence 3, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; FILE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-0333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-3

Query Match 98.0%; Score 1182; DB 3; Length 530;
Best Local Similarity 99.6%; Pred. No. 6.1e-125;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 5 QLOSVSSAIHLCDKKKMWELSLNIPVNHGPOEESCGSSQLHENS GSPETSRSLPAPQDNDF 64
Db 303 KLOSVSSAIHLCDKKKMWELSLNIPVNHGPOEESCGSSQLHENS GSPETSRSLPAPQDNDF 362
QY 65 LSRKAQDCYFMKLHHCPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124
Db 363 LSRKAQDCYFMKLHHCPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 422
QY 125 PGIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
Db 423 PGIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 482
QY 185 TTDIOGEEFAKVIQVKLKNQKMGLOQYPPEILVVSRSPLNLLQNKSM 232

Db 483 TTDIOGEEFAKVIQVKLKNQKMGLOQYPPEILVVSRSPLNLLQNKSM 530

RESULT 4
US-09-069-023-1
; Sequence 1, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; FILE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-0333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 531
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-1

Query Match 98.0%; Score 1182; DB 3; Length 531;
Best Local Similarity 99.6%; Pred. No. 6.1e-125;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 5 QLOSVSSAIHLCDKKKMWELSLNIPVNHGPOEESCGSSQLHENS GSPETSRSLPAPQDNDF 64
Db 304 KLOSVSSAIHLCDKKKMWELSLNIPVNHGPOEESCGSSQLHENS GSPETSRSLPAPQDNDF 363
QY 65 LSRKAQDCYFMKLHHCPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124
Db 364 LSRKAQDCYFMKLHHCPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 423
QY 125 PGIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
Db 424 PGIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 483
QY 185 TTDIOGEEFAKVIQVKLKNQKMGLOQYPPEILVVSRSPLNLLQNKSM 232
Db 484 TTDIOGEEFAKVIQVKLKNQKMGLOQYPPEILVVSRSPLNLLQNKSM 531

RESULT 5
US-09-069-023-27
; Sequence 27, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; FILE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-0333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-27

Query Match 98.0%; Score 1182; DB 3; Length 540;
Best Local Similarity 99.6%; Pred. No. 6.3e-125;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 5 QLOSVSSAIHLCDKKKMWELSLNIPVNHGPOEESCGSSQLHENS GSPETSRSLPAPQDNDF 64
Db 313 KLOSVSSAIHLCDKKKMWELSLNIPVNHGPOEESCGSSQLHENS GSPETSRSLPAPQDNDF 372

QY 65 LSRKAQDCYFMKLHCPGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124
Db 373 LSRKAQDCYFMKLHCPGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 432
QY 125 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
Db 433 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492
QY 185 TTIOGEEFAKVIQKLKONKQWGLQPYPEILVVSRSPLNLLQKSM 232
Db 493 TTIOGEEFAKVIQKLKONKQWGLQPYPEILVVSRSPLNLLQKSM 540

RESULT 6

US-09-345-473E-28
; Sequence 28, Application US/09345473E
; Patent No. 6558903
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin
; TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof
; FILE REFERENCE: 35800/183781
; CURRENT APPLICATION NUMBER: US/09/345,473E
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-345-473E-28

Query Match 98.0%; Score 1182; DB 4; Length 540;
Best Local Similarity 99.6%; Pred. No. 6.3e-125;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 QLOSVSSAIHLCDKKKMWELSLNIPVNHGPOEESCGSSQLHENGSPETSRSLPAPQDNDF 64
Db 313 KLOSVSSAIHLCDKKKMWELSLNIPVNHGPOEESCGSSQLHENGSPETSRSLPAPQDNDF 372
QY 65 LSRKAQDCYFMKLHCPGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124
Db 373 LSRKAQDCYFMKLHCPGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 432
QY 125 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
Db 433 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492
QY 185 TTIOGEEFAKVIQKLKONKQWGLQPYPEILVVSRSPLNLLQKSM 232
Db 493 TTIOGEEFAKVIQKLKONKQWGLQPYPEILVVSRSPLNLLQKSM 540

RESULT 7

US-09-019-942-1
; Sequence 1, Application US/09019942
; Patent No. 6033855
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
; TITLE OF INVENTION: DOMAIN POLYPEPTIDES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95

SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,942
FILING DATE: 06-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/068001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-019-942-1

Query Match 97.5%; Score 1176; DB 3; Length 540;
Best Local Similarity 99.1%; Pred. No. 3e-124;
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLOSVSSAIHLCDKKKMWELSLNIPVNHGPOEESCGSSQLHENGSPETSRSLPAPQDNDF 64
Db 313 KLOSVSSAIHLCDKKKMWELSLNIPVNHGPOEESCGSSQLHENGSPETSRSLPAPQDNDF 372
QY 65 LSRKAQDCYFMKLHCPGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124
Db 373 LSRKAQDCYFMKLHCPGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 432
QY 125 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
Db 433 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492
QY 185 TTIOGEEFAKVIQKLKONKQWGLQPYPEILVVSRSPLNLLQKSM 232
Db 493 TTIOGEEFAKVIQKLKONKQWGLQPYPEILVVSRSPLNLLQKSM 540

RESULT 8

US-09-099-041A-2
; Sequence 2, Application US/09099041A
; Patent No. 6340576
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/09/099,041A
; CURRENT FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-099-041A-2

Query Match 97.5%; Score 1176; DB 3; Length 540;
Best Local Similarity 99.1%; Pred. No. 3e-124;
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLOSVSSAIHLCDKKKMWELSLNIPVNHGPOEESCGSSQLHENGSPETSRSLPAPQDNDF 64
Db 313 KLOSVSSAIHLCDKKKMWELSLNIPVNHGPOEESCGSSQLHENGSPETSRSLPAPQDNDF 372

QY 65 LSRKAQDCYFMKLHCPGNHSDSTISGSORAAFCDHKTTPCSSLINPLSTAGNSRLQ 124
Db 373 LSRKAQDCYFMKLHCPGNHSDSTISGSORAAFCDHKTTPCSSLINPLSTAGNSRLQ 432
QY 125 PGIAQOWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
Db 433 PGIAQOWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492
QY 185 TTIDQEEFAKVIQKLDKQKQGLQPYPEILVWSRSPSLNLLQKSM 232
Db 493 TTIDQEEFAKVIQKLDKQKQGLQPYPEILVWSRSPSLNLLQKSM 540

RESULT 9

US-09-245-281-2
; Sequence 2, Application US/09245281
; Patent No. 6369196
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/09/245,281
; EARLIER FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: US 09/207,359
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: US 09/099,041
; EARLIER FILING DATE: 1998-06-17
; EARLIER APPLICATION NUMBER: US 09/019,942
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-245-281-2

Query Match 97.5%; Score 1176; DB 3; Length 540;
Best Local Similarity 99.1%; Pred. No. 3e-124;
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLOSVSSAIHLCDKXKMWELSLNIPVNHGPOBESCGSSQLHNSGSPETSRSLPAPQDNDF 64
Db 313 QLOSVSSAIHLCDKXKMWELSLNIPVNHGPOBESCGSSQLHNSGSPETSRSLPAPQDNDF 372
QY 65 LSRKAQDCYFMKLHCPGNHSDSTISGSORAAFCDHKTTPCSSLINPLSTAGNSRLQ 124
Db 373 LSRKAQDCYFMKLHCPGNHSDSTISGSORAAFCDHKTTPCSSLINPLSTAGNSRLQ 432
QY 125 PGIAQOWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
Db 433 PGIAQOWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492
QY 185 TTIDQEEFAKVIQKLDKQKQGLQPYPEILVWSRSPSLNLLQKSM 232
Db 493 TTIDQEEFAKVIQKLDKQKQGLQPYPEILVWSRSPSLNLLQKSM 540

RESULT 10

US-09-470-271-1
; Sequence 1, Application US/09470271
; Patent No. 6410689
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
; TITLE OF INVENTION: DOMAIN POLYPEPTIDES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA

; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/470,271
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/019,942
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meikiejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/068001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 540 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-470-271-1

Query Match 97.5%; Score 1176; DB 4; Length 540;
Best Local Similarity 99.1%; Pred. No. 3e-124;
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLOSVSSAIHLCDKXKMWELSLNIPVNHGPOBESCGSSQLHNSGSPETSRSLPAPQDNDF 64
Db 313 QLOSVSSAIHLCDKXKMWELSLNIPVNHGPOBESCGSSQLHNSGSPETSRSLPAPQDNDF 372
QY 65 LSRKAQDCYFMKLHCPGNHSDSTISGSORAAFCDHKTTPCSSLINPLSTAGNSRLQ 124
Db 373 LSRKAQDCYFMKLHCPGNHSDSTISGSORAAFCDHKTTPCSSLINPLSTAGNSRLQ 432
QY 125 PGIAQOWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
Db 433 PGIAQOWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492
QY 185 TTIDQEEFAKVIQKLDKQKQGLQPYPEILVWSRSPSLNLLQKSM 232
Db 493 TTIDQEEFAKVIQKLDKQKQGLQPYPEILVWSRSPSLNLLQKSM 540

RESULT 11

US-09-207-359B-2
; Sequence 2, Application US/09207359B
; Patent No. 6469140
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/207,359B
; CURRENT FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-207-359B-2

Query Match 97.5%; Score 1176; DB 4; Length 540;
Best Local Similarity 99.1%; Pred. No. 3e-124;
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLOSVSSAIHLCDKKKMWELSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 64
:|||||
DB 313 KLOSVSSAIHLCDKKKMWELSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 372
:|||||
QY 65 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKHTTPCSSAINPLSTAGNSERLQ 124
:|||||
DB 373 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKHTTPCSSAINPLSTAGNSERLQ 432
:|||||
QY 125 PGIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
:|||||
DB 433 PGIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492
:|||||
QY 185 TTIOQEEFAKVIQVKLKDKNQKGLQPYPEILVVSRSPSLNLLQNKSM 232
:|||||
DB 493 TTIOQEEFAKVIQVKLKDKNQKGLQPYPEILVVSRSPSLNLLQNKSM 540
:|||||

RESULT 12
US-09-340-620A-2.
; Sequence 2, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/340,620A
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-340-620A-2

Query Match 97.5%; Score 1176; DB 4; Length 540;
Best Local Similarity 99.1%; Pred. No. 3e-124;
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLOSVSSAIHLCDKKKMWELSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 64
:|||||
DB 313 KLOSVSSAIHLCDKKKMWELSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 372
:|||||
QY 65 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKHTTPCSSAINPLSTAGNSERLQ 124
:|||||
DB 373 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKHTTPCSSAINPLSTAGNSERLQ 432
:|||||
QY 125 PGIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
:|||||
DB 433 PGIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492
:|||||
QY 185 TTIOQEEFAKVIQVKLKDKNQKGLQPYPEILVVSRSPSLNLLQNKSM 232
:|||||
DB 493 TTIOQEEFAKVIQVKLKDKNQKGLQPYPEILVVSRSPSLNLLQNKSM 540
:|||||

RESULT 13
US-09-865-364-2
; Sequence 2, Application US/09865364
; Patent No. 6613521
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-316001
; CURRENT APPLICATION NUMBER: US/09/865,364
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-865-364-2

APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-112001
CURRENT APPLICATION NUMBER: US/09/865,364
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/207,359
PRIOR FILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 540
TYPE: PRT
ORGANISM: Homo sapiens
US-09-865-364-2

Query Match 97.5%; Score 1176; DB 4; Length 540;
Best Local Similarity 99.1%; Pred. No. 3e-124; 1; Indels 0; Gaps 0;
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLOSVSSAIHLCDKKKMWELSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 64
:|||||
DB 313 KLOSVSSAIHLCDKKKMWELSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 372
:|||||
QY 65 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKHTTPCSSAINPLSTAGNSERLQ 124
:|||||
DB 373 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKHTTPCSSAINPLSTAGNSERLQ 432
:|||||
QY 125 PGIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
:|||||
DB 433 PGIAQOWIQSKREDIVNQMTACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492
:|||||
QY 185 TTIOQEEFAKVIQVKLKDKNQKGLQPYPEILVVSRSPSLNLLQNKSM 232
:|||||
DB 493 TTIOQEEFAKVIQVKLKDKNQKGLQPYPEILVVSRSPSLNLLQNKSM 540
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RESULT 14
US-09-748-537-1
; Sequence 1, Application US/09748537
; Patent No. 6680167
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Chao, Moses V.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-316001
; CURRENT APPLICATION NUMBER: US/09/748,537
; CURRENT FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-748-537-1

Query Match 97.5%; Score 1176; DB 4; Length 540;
Best Local Similarity 99.1%; Pred. No. 3e-124; 1; Indels 0; Gaps 0;
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLOSVSSAIHLCDKKKMWELSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 64
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DB 313 KLOSVSSAIHLCDKKKMWELSLNIPVNHGPOEESCGSSQLHNSGSPETSRLPAPQDNDF 372
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QY 65 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKHTTPCSSAINPLSTAGNSERLQ 124
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Db 373 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTIPCSSAIINPLSTAGNSERLQ 432
QY 125 PGIAQOWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
Db 433 PGIAQOWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492
QY 185 TTDIQGEFAKVIQKLDKNQKMGLOPYPEILVVSRSPSLNLLQKSM 232
Db 493 TTDIQGEFAKVIQKLDKNQKMGLOPYPEILVVSRSPSLNLLQKSM 540
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RESULT 15

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US-09-069-023-6
; Sequence 6, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-0333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-6
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Query Match 71.9%; Score 867; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 4.9e-90;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 SRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTIPCSSAIINPLSTAGNSERLQ 125
Db 1 SRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTIPCSSAIINPLSTAGNSERLQ 60

QY 126 GIAQOWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 185
Db 61 GIAQOWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 120

QY 186 TTDIQGEFAKVIQKLDKNQKMGLOPYPEILVVSRSPSLNLLQKSM 232
Db 121 TTDIQGEFAKVIQKLDKNQKMGLOPYPEILVVSRSPSLNLLQKSM 167
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Search completed: January 28, 2005, 13:08:45
Job time : 40 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 28, 2005, 13:00:33 ; Search time 146 Seconds
(without alignments)
574.104 Million cell updates/sec

Title: US-09-771-161A-93

Perfect score: 1206

Sequence: 1 MYSLQIQSVSSAIHLCDKKK.....PEILVVSRSPLNLLQNKSM 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 segs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1206	100.0	232	9	US-09-771-161A-93
2	1182	98.0	540	9	US-09-771-161A-184
3	1182	98.0	540	9	US-09-862-027-28
4	1182	98.0	540	10	US-09-981-397A-14
5	1182	98.0	540	17	US-10-825-282-36
6	1182	98.0	544	9	US-09-925-301-1015
7	1176	97.5	540	9	US-09-748-537-1
8	1176	97.5	540	9	US-09-728-721-2
9	1176	97.5	540	13	US-10-133-780-1
10	1176	97.5	540	13	US-10-105-931-2
11	1176	97.5	540	13	US-10-118-984-2
12	1176	97.5	540	14	US-10-295-981-2
13	632	52.4	131	9	US-09-728-721-5

14	632	52.4	131	13	US-10-105-931-5	Sequence 5, Appli
15	632	52.4	131	13	US-10-118-984-5	Sequence 5, Appli
16	632	52.4	131	14	US-10-295-981-5	Sequence 5, Appli
17	544	45.1	109	9	US-09-728-721-6	Sequence 6, Appli
18	544	45.1	109	13	US-10-105-931-6	Sequence 6, Appli
19	544	45.1	109	13	US-10-118-984-6	Sequence 6, Appli
20	544	45.1	109	14	US-10-295-981-6	Sequence 6, Appli
21	461	38.2	92	13	US-10-014-269-21	Sequence 21, Appli
22	461	38.2	92	13	US-10-002-974-21	Sequence 21, Appli
23	461	38.2	92	14	US-10-314-506-21	Sequence 21, Appli
24	451	37.4	90	9	US-09-841-879B-10	Sequence 10, Appli
25	451	37.4	90	16	US-10-756-097-10	Sequence 10, Appli
26	447	37.1	89	9	US-09-931-071-11	Sequence 11, Appli
27	149.5	12.4	109	9	US-09-728-721-71	Sequence 71, Appli
28	149.5	12.4	109	14	US-10-295-981-71	Sequence 71, Appli
29	143.5	11.9	95	9	US-09-841-879B-12	Sequence 12, Appli
30	143.5	11.9	95	16	US-10-756-097-12	Sequence 12, Appli
31	122.5	10.2	164	9	US-09-728-721-41	Sequence 41, Appli
32	122.5	10.2	164	13	US-10-118-984-41	Sequence 41, Appli
33	122.5	10.2	164	14	US-10-295-981-41	Sequence 41, Appli
34	122.5	10.2	249	9	US-09-728-721-39	Sequence 39, Appli
35	122.5	10.2	249	13	US-10-118-984-39	Sequence 39, Appli
36	122.5	10.2	249	14	US-10-295-981-39	Sequence 39, Appli
37	122.5	10.2	507	14	US-10-401-194-3	Sequence 3, Appli
38	122.5	10.2	953	9	US-09-728-721-8	Sequence 8, Appli
39	122.5	10.2	953	13	US-10-105-931-8	Sequence 8, Appli
40	122.5	10.2	953	13	US-10-118-984-8	Sequence 8, Appli
41	122.5	10.2	953	14	US-10-013-477-12	Sequence 12, Appli
42	122.5	10.2	953	14	US-10-295-981-8	Sequence 8, Appli
43	122.5	10.2	953	14	US-10-028-374-4	Sequence 4, Appli
44	122.5	10.2	953	14	US-10-183-770-4	Sequence 4, Appli
45	119	9.9	100	9	US-09-728-721-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1

US-09-771-161A-93
; Sequence 93, Application US/09771161A
; Patent No. US0020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 93
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-93

Query Match 100.0%; Score 1206; DB 9; Length 232;
Best Local Similarity 100.0%; Pred. No. 2.8e-107;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MYSLQIQSVSSAIHLCDKKKMLSLNIPVNHGQEESSGSSQLHNSGSPETSRSLPAPQ 60	
Db	1	MYSLQIQSVSSAIHLCDKKKMLSLNIPVNHGQEESSGSSQLHNSGSPETSRSLPAPQ 60	
QY	61	DNDFLSRKAQDCYFMKLHHCPCGNHSDSTISSQRAAFCDHKHTTPCSSLINPLSTAGNS 120	
Db	61	DNDFLSRKAQDCYFMKLHHCPCGNHSDSTISSQRAAFCDHKHTTPCSSLINPLSTAGNS 120	

QY 121 ERLQPGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVR 180
Db 121 ERLQPGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVR 180
QY 181 QLLDTTDIOGEEFAKVIQVOKLKDKNQKMGLOPYPEILVWRSPLNLLQNKSM 232
Db 181 QLLDTTDIOGEEFAKVIQVOKLKDKNQKMGLOPYPEILVWRSPLNLLQNKSM 232

RESULT 2

US-09-771-161A-184
; Sequence 184, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 184
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-184

Query Match 98.0%; Score 1182; DB 9; Length 540;
Best Local Similarity 99.6%; Pred. No. 1.8e-104;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 QLOSVSSAIHLCDKKKMWLSLNI PVNHGPOEESCGSSQLHENSQSPETSRSLPAPQDNDF 64
Db 313 KLOSVSSAIHLCDKKKMWLSLNI PVNHGPOEESCGSSQLHENSQSPETSRSLPAPQDNDF 372

QY 65 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSLINPLSTAGNSERLQ 124
Db 373 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSLINPLSTAGNSERLQ 432

QY 125 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
Db 433 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492

QY 185 TTDIOGEEFAKVIQVOKLKDKNQKMGLOPYPEILVWRSPLNLLQNKSM 232
Db 493 TTDIOGEEFAKVIQVOKLKDKNQKMGLOPYPEILVWRSPLNLLQNKSM 540

RESULT 3

US-09-862-027-28
; Sequence 28, Application US/09862027
; Patent No. US20020142428A1
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; TITLE OF INVENTION: No. US20020142428A1el Kinases and Uses Thereof
; FILE REFERENCE: 35800/234862
; CURRENT APPLICATION NUMBER: US/09/862,027
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 09/345,473
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-862-027-28

Query Match 98.0%; Score 1182; DB 9; Length 540;
Best Local Similarity 99.6%; Pred. No. 1.8e-104;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 QLOSVSSAIHLCDKKKMWLSLNI PVNHGPOEESCGSSQLHENSQSPETSRSLPAPQDNDF 64
Db 313 KLOSVSSAIHLCDKKKMWLSLNI PVNHGPOEESCGSSQLHENSQSPETSRSLPAPQDNDF 372

QY 65 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSLINPLSTAGNSERLQ 124
Db 373 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSLINPLSTAGNSERLQ 432

QY 125 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
Db 433 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492

QY 185 TTDIOGEEFAKVIQVOKLKDKNQKMGLOPYPEILVWRSPLNLLQNKSM 232
Db 493 TTDIOGEEFAKVIQVOKLKDKNQKMGLOPYPEILVWRSPLNLLQNKSM 540

RESULT 4

US-09-981-397A-14
; Sequence 14, Application US/09981397A
; Publication No. US20030082519A1
; GENERAL INFORMATION:
; APPLICANT: Axixima Pharmaceuticals AG
; APPLICANT: Schubart, Daniel
; APPLICANT: Habenberger, Peter
; APPLICANT: Stein-Gerlach, Matthias
; APPLICANT: Bevec, Dorian
; TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their
; TITLE OF INVENTION: Inhibition
; FILE REFERENCE: AXM-004.1 US
; CURRENT APPLICATION NUMBER: US/09/981,397A
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/240,750
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-981-397A-14

Query Match 98.0%; Score 1182; DB 10; Length 540;
Best Local Similarity 99.6%; Pred. No. 1.8e-104;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 QLOSVSSAIHLCDKKKMWLSLNI PVNHGPOEESCGSSQLHENSQSPETSRSLPAPQDNDF 64
Db 313 KLOSVSSAIHLCDKKKMWLSLNI PVNHGPOEESCGSSQLHENSQSPETSRSLPAPQDNDF 372

QY 65 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSLINPLSTAGNSERLQ 124
Db 373 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSLINPLSTAGNSERLQ 432

QY 125 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
Db 433 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492

QY 185 TTDIOGEEFAKVIQVOKLKDKNQKMGLOPYPEILVWRSPLNLLQNKSM 232
Db 493 TTDIOGEEFAKVIQVOKLKDKNQKMGLOPYPEILVWRSPLNLLQNKSM 540

RESULT 5

US-10-825-282-36
; Sequence 36, Application US/10825282
; Publication No. US20040224389A1
; GENERAL INFORMATION:

APPLICANT: 3921-1-1-1
TITLE OF INVENTION: VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND
METHODS FOR MAKING AND USING THE SAME
FILE REFERENCE: 3921-1-1-1
CURRENT APPLICATION NUMBER: US/10/825,282
CURRENT FILING DATE: 2004-04-14
PRIOR APPLICATION NUMBER: US/09/456,357
PRIOR FILING DATE: 1999-12-08
PRIOR APPLICATION NUMBER: 60/134,416
PRIOR FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: 09/087,195
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: 08/378,507
PRIOR FILING DATE: 1995-01-26
PRIOR APPLICATION NUMBER: 08/250,478
PRIOR FILING DATE: 1994-05-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 36
LENGTH: 540
TYPE: PRT
ORGANISM: Homo sapiens
US-10-825-282-36

Query Match 98.0%; Score 1182; DB 17; Length 540;
Best Local Similarity 99.6%; Pred. No. 1.8e-104;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 5 QLOSVSSAIHLCDKKKMWLSLNPVNHGPQEESSGSSQLHNSGSPETSRSLPAPQDNDF 64
DB 313 QLOSVSSAIHLCDKKKMWLSLNPVNHGPQEESSGSSQLHNSGSPETSRSLPAPQDNDF 372
QY 65 LSRKAQDCYFMKLHHCPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124
DB 373 LSRKAQDCYFMKLHHCPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 432
QY 125 PGIAQOWIOSKREDIVNQMTACLNSQLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
DB 433 PGIAQOWIOSKREDIVNQMTACLNSQLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492
QY 185 TTDIQGEFAKIVQKLKDKNQKQGLQPYPEILVWRSRPSLNLQKSM 232
DB 493 TTDIQGEFAKIVQKLKDKNQKQGLQPYPEILVWRSRPSLNLQKSM 540

RESULT 6
US-09-925-301-1015
Sequence 1015, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1015
LENGTH: 544
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-301-1015

Query Match 98.0%; Score 1182; DB 9; Length 544;
Best Local Similarity 99.6%; Pred. No. 1.8e-104;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 5 QLOSVSSAIHLCDKKKMWLSLNPVNHGPQEESSGSSQLHNSGSPETSRSLPAPQDNDF 64

DB 317 QLOSVSSAIHLCDKKKMWLSLNPVNHGPQEESSGSSQLHNSGSPETSRSLPAPQDNDF 376
QY 65 LSRKAQDCYFMKLHHCPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124
DB 377 LSRKAQDCYFMKLHHCPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 436
QY 125 PGIAQOWIOSKREDIVNQMTACLNSQLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
DB 437 PGIAQOWIOSKREDIVNQMTACLNSQLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 496
QY 185 TTDIQGEFAKIVQKLKDKNQKQGLQPYPEILVWRSRPSLNLQKSM 232
DB 497 TTDIQGEFAKIVQKLKDKNQKQGLQPYPEILVWRSRPSLNLQKSM 544

RESULT 7
US-09-748-537-1
Sequence 1, Application US/09748537
Patent No. US20020061833A1
GENERAL INFORMATION:
APPLICANT: Bertin, John
APPLICANT: Chao, Moses V.
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-316001
CURRENT APPLICATION NUMBER: US/09/748,537
CURRENT FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 540
TYPE: PRT
ORGANISM: Homo sapiens
US-09-748-537-1

Query Match 97.5%; Score 1176; DB 9; Length 540;
Best Local Similarity 99.1%; Pred. No. 6.9e-104;
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 5 QLOSVSSAIHLCDKKKMWLSLNPVNHGPQEESSGSSQLHNSGSPETSRSLPAPQDNDF 64
DB 313 QLOSVSSAIHLCDKKKMWLSLNPVNHGPQEESSGSSQLHNSGSPETSRSLPAPQDNDF 372
QY 65 LSRKAQDCYFMKLHHCPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124
DB 373 LSRKAQDCYFMKLHHCPCGNHSDSTISGSORAAFCDHKTTPCSSAIINPLSTAGNSERLQ 432
QY 125 PGIAQOWIOSKREDIVNQMTACLNSQLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
DB 433 PGIAQOWIOSKREDIVNQMTACLNSQLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492
QY 185 TTDIQGEFAKIVQKLKDKNQKQGLQPYPEILVWRSRPSLNLQKSM 232
DB 493 TTDIQGEFAKIVQKLKDKNQKQGLQPYPEILVWRSRPSLNLQKSM 540

RESULT 8
US-09-728-721-2
Sequence 2, Application US/09728721
Patent No. US20020061845A1
GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-124001
CURRENT APPLICATION NUMBER: US/09/728,721
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: 09/340,620
PRIOR FILING DATE: 1999-06-28
PRIOR APPLICATION NUMBER: US 09/207,359
PRIOR FILING DATE: 1998-12-08

```
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-728-721-2

Query Match          97.5%; Score 1176; DB 9; Length 540;
Best Local Similarity 99.1%; Pred. No. 6.9e-104;
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLQSVSSAIHLCDKKKMWELSLNIPVNHGQPEESCGSSQLHENSGLSPETSRLPAPQDNDF 64
Db 313 QLQSVSSAIHLCDKKKMWELSLNIPVNHGQPEESCGSSQLHENSGLSPETSRLPAPQDNDF 372

QY 65 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124
Db 373 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 432

QY 125 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
Db 433 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492

QY 185 TTDIQEEFAKIVQKLKDKNQMGLOPYPEILVWSRSPSLNLLQNKSM 232
Db 493 TTDIQEEFAKIVQKLKDKNQMGLOPYPEILVWSRSPSLNLLQNKSM 540

RESULT 9
US-10-133-780-1
; Sequence 1, Application US/10133780
; Publication No. US20020123115A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
; DOMAIN POLYPEPTIDES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/133,780
; FILING DATE: 26-Apr-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/019,942
; FILING DATE: 06-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: 07334/068001
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 540 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-133-780-1

Query Match          97.5%; Score 1176; DB 13; Length 540;
Best Local Similarity 99.1%; Pred. No. 6.9e-104;
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLQSVSSAIHLCDKKKMWELSLNIPVNHGQPEESCGSSQLHENSGLSPETSRLPAPQDNDF 64
Db 313 QLQSVSSAIHLCDKKKMWELSLNIPVNHGQPEESCGSSQLHENSGLSPETSRLPAPQDNDF 372

QY 65 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124
Db 373 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 432

QY 125 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
Db 433 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492

QY 185 TTDIQEEFAKIVQKLKDKNQMGLOPYPEILVWSRSPSLNLLQNKSM 232
Db 493 TTDIQEEFAKIVQKLKDKNQMGLOPYPEILVWSRSPSLNLLQNKSM 540

RESULT 10
US-10-105-931-2
; Sequence 2, Application US/10105931
; Publication No. US20020150987A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/10/105,931
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-105-931-2

Query Match          97.5%; Score 1176; DB 13; Length 540;
Best Local Similarity 99.1%; Pred. No. 6.9e-104;
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLQSVSSAIHLCDKKKMWELSLNIPVNHGQPEESCGSSQLHENSGLSPETSRLPAPQDNDF 64
Db 313 QLQSVSSAIHLCDKKKMWELSLNIPVNHGQPEESCGSSQLHENSGLSPETSRLPAPQDNDF 372

QY 65 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 124
Db 373 LSRKAQDCYFMKLHHCPCGNHSDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQ 432

QY 125 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 184
Db 433 PGIAQOWIOSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLD 492

QY 185 TTDIQEEFAKIVQKLKDKNQMGLOPYPEILVWSRSPSLNLLQNKSM 232
Db 493 TTDIQEEFAKIVQKLKDKNQMGLOPYPEILVWSRSPSLNLLQNKSM 540

RESULT 11
US-10-118-984-2
; Sequence 2, Application US/10118984
; Publication No. US20020197693A1
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Tue Feb 1 09:12:09 2005

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; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-931-5

Query Match      52.4%; Score 632; DB 13; Length 131;
Best Local Similarity 98.3%; Pred. No. 1.6e-52;
Matches 117; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      5 QLOSVSSAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDF 64
      :|||||
DB      13 KLOSVSSAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDF 72
      :|||||

QY      65 LSRKAQDCYFMKLHHCPCGNHSDSTISSQRAAFCDHKTTPCSSAIINPLSTAGNSERL 123
      :|||||
DB      73 LSRKAQDCYFMKLHHCPCGNHSDSTISSQRAAFCDHKTTPCSSAIINPLSTAGNSERL 131
      :|||||
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RESULT 15
US-10-118-984-5
; Sequence 5, Application US/10118984
; Publication No. US20020197693A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/10/118,984
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-118-984-5
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Query Match      52.4%; Score 632; DB 13; Length 131;
Best Local Similarity 98.3%; Pred. No. 1.6e-52;
Matches 117; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      5 QLOSVSSAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDF 64
      :|||||
DB      13 KLOSVSSAIHLCDKKKMLSLNIPVNHGPOEESCGSSQLHNSGSPETSRSLPAPQDNDF 72
      :|||||

QY      65 LSRKAQDCYFMKLHHCPCGNHSDSTISSQRAAFCDHKTTPCSSAIINPLSTAGNSERL 123
      :|||||
DB      73 LSRKAQDCYFMKLHHCPCGNHSDSTISSQRAAFCDHKTTPCSSAIINPLSTAGNSERL 131
      :|||||
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Search completed: January 28, 2005, 13:19:48
Job time : 147 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model
Run on: January 31, 2005, 23:05:56 ; Search time 103 Seconds
(without alignments)
1601.000 Million cell updates/sec

Title: US-09-771-161A-93
Perfect score: 1206
Sequence: 1 MYSLOQVSSAIHLCDKKK.....PEILVVSRLNLLQKSM 232

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues
Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool_h/US09771161/runat_28012005_103459_5/app_query.fasta_1.391
-DB=Issued_Patents_NA -QFMT=fstetp -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09771161 @Cgn 1.1.69 @runat 28012005_103459_5 -NCPU=6 -ICPU=3 -NO_MMWP
-LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
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5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1182	98.0	2501	4	US-09-920-663-3
2	1182	98.0	2502	3	US-09-069-023-2
3	1176	97.5	1620	3	US-09-099-041A-3
4	1176	97.5	1620	3	US-09-245-281-3
5	1176	97.5	1620	4	US-09-207-359B-3
6	1176	97.5	1620	4	US-09-340-620A-3
7	1176	97.5	1620	4	US-09-865-364-3
8	1176	97.5	1931	3	US-09-019-942-2
9	1176	97.5	1931	3	US-09-099-041A-1
10	1176	97.5	1931	3	US-09-245-281-1
11	1176	97.5	1931	4	US-09-470-271-2
12	1176	97.5	1931	4	US-09-207-359B-1

13	1176	97.5	1931	4	US-09-340-620A-1	Sequence 1, Appli
14	1176	97.5	1931	4	US-09-865-364-1	Sequence 1, Appli
15	1176	97.5	1931	4	US-09-748-537-2	Sequence 2, Appli
16	1165	96.6	1060	4	US-09-023-655-684	Sequence 684, App
17	125	10.4	1400	3	US-09-245-281-40	Sequence 40, Appl
18	125	10.4	1400	4	US-09-207-359B-40	Sequence 40, Appl
19	125	10.4	1400	4	US-09-340-620A-40	Sequence 40, Appl
20	125	10.4	1400	4	US-09-865-364-40	Sequence 40, Appl
21	125	10.4	1400	4	US-09-099-041A-7	Sequence 7, Appli
22	125	10.4	1400	4	US-09-245-281-7	Sequence 7, Appli
23	125	10.4	1400	4	US-09-207-359B-7	Sequence 7, Appli
24	125	10.4	1400	4	US-09-340-620A-7	Sequence 7, Appli
25	125	10.4	1400	4	US-09-865-364-7	Sequence 7, Appli
26	125	10.4	1400	4	US-09-245-281-38	Sequence 38, Appl
27	125	10.4	1400	4	US-09-207-359B-38	Sequence 38, Appl
28	125	10.4	1400	4	US-09-340-620A-38	Sequence 38, Appl
29	125	10.4	1400	4	US-09-865-364-38	Sequence 38, Appl
30	122.5	10.2	2859	3	US-09-099-041A-9	Sequence 9, Appli
31	122.5	10.2	2859	3	US-09-245-281-9	Sequence 9, Appli
32	122.5	10.2	2859	4	US-09-207-359B-9	Sequence 9, Appli
33	122.5	10.2	2859	4	US-09-340-620A-9	Sequence 9, Appli
34	122.5	10.2	2859	4	US-09-865-364-9	Sequence 9, Appli
35	104.5	8.7	626	3	US-09-019-942-4	Sequence 4, Appli
36	104.5	8.7	626	4	US-09-470-271-4	Sequence 4, Appli
37	104.5	8.7	626	4	US-09-748-537-4	Sequence 4, Appli
38	104.5	8.7	1470	3	US-09-099-041A-27	Sequence 27, Appl
39	104.5	8.7	1470	3	US-09-245-281-27	Sequence 27, Appl
40	104.5	8.7	1470	4	US-09-207-359B-27	Sequence 27, Appl
41	104.5	8.7	1470	4	US-09-340-620A-27	Sequence 27, Appl
42	104.5	8.7	1470	4	US-09-865-364-27	Sequence 27, Appl
43	104.5	8.7	3080	3	US-09-099-041A-25	Sequence 25, Appl
44	104.5	8.7	3080	3	US-09-245-281-25	Sequence 25, Appl
45	104.5	8.7	3080	4	US-09-207-359B-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-09-920-663-3
; Sequence 3, Application US/09920663
; Patent No. 6426221
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Donna T. Ward
; TITLE OF INVENTION: ANTISENSE MODULATION OF RIP2 EXPRESSION
; FILE REFERENCE: RTS-0233
; CURRENT APPLICATION NUMBER: US/09/920,663
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 3
; LENGTH: 2501
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (225)...(1847)
US-09-920-663-3

Alignment Scores:
Pred. No.: 3.35e-138 Length: 2501
Score: 1182.00 Matches: 227
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.56% Mismatches: 0
Query Match: 98.01% Indels: 0
DB: 4 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-920-663-3 (1-2501)

QY	5	GinLeuGlnSerValSerSerhlatleHisLeuCyeAspIyalyIyMetGluLeuSer	24
Db	1161	AAAGTTACAGAGTGTTCACAGTCCATTCACCTATGTGACAAAGAAATGGAATATCT	1320
QY	25	LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis	44

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Db      1221 CTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGGGATCTCTCAGCTCCAT 1280
QY      45  GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
Db      1281 GAAATAGTGGTCTCTGAAACTTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTT 1340
QY      65  LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84
Db      1341 TTATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTCTCTGGAATCAC 1400
QY      85  SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
Db      1401 AGTGGGATAGACCACTTCTCGTCTCAAGGGCTGCATCTGTGATCACAAGCACT 1460
QY      105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
Db      1461 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAG 1520
QY      125 ProGlyIleAlaGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
Db      1521 CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACA 1580
QY      145  GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
Db      1581 GAAGCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGAG 1640
QY      165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
Db      1641 GACTATGAATCTGTAGTACCAAGCCTACAGGACCTCAAAAGTTCAGACAATTTACTAGAC 1700
QY      185 ThrThrAspIleGlnGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
Db      1701 ACTACTGACATCCAGGGAAGAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAAC 1760
QY      205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
Db      1761 AAACAAATGGGCTTCAGCCCTTACCCGGAATACTTGTGGTTCTAGATCACAATCTTTA 1820
QY      225 AsnLeuLeuGlnAsnLysSerMet 232
Db      1821 AATTTACTTCAAAATAAAAGCATG 1844

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RESULT 2

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US-09-069-023-2
; Sequence 2, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069, 023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-069-023-2

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Alignment Scores:
Pred. No.: 3,35e-138 Length: 2502
Score: 1182.00 Matches: 227
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.56% Mismatches: 0
Query Match: 98.01% Indels: 0
DB: 3 Gaps: 0

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US-09-771-161A-93 (1-232) x US-09-069-023-2 (1-2502)

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QY      5  GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24
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QY      25  LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
Db      1222 CTGAACATACCTGTAAATCATGGTCCACAAGAGGAATCATGGGATCTCTCAGCTCCAT 1281
QY      45  GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
Db      1282 GAAATAGTGGTCTCTCGTCTCAAGGCTCCCTGCCAGCTCCTCAAGACAATGATTTT 1341
QY      65  LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84
Db      1342 TTATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTCTCTGGAATCAC 1401
QY      85  SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
Db      1402 AGTTGGGATAGCACCATTCTCGTCTCAAGGGCTGCATTCGTGATCACAAGCACT 1461
QY      105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
Db      1462 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAG 1521
QY      125 ProGlyIleAlaGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
Db      1522 CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACA 1581
QY      145  GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
Db      1582 GAAGCTGCTTAAACAGTCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGAG 1641
QY      165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
Db      1642 GACTATGAATCTGTAGTACCAAGCCTCAAGGACCTCAAAAGTTCAGACAATTTACTAGAC 1701
QY      185 ThrThrAspIleGlnGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
Db      1702 ACTACTGACATCCAGGGAAGAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAAC 1761
QY      205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
Db      1762 AAACAAATGGGCTTTCAGCCCTTACCCGGAATACTTGTGGTTCTAGATCACAATCTTTA 1821
QY      225 AsnLeuLeuGlnAsnLysSerMet 232
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RESULT 3

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US-09-099-041A-3
; Sequence 3, Application US/09099041A
; Patent No. 6340576
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/09/099, 041A
; CURRENT FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019, 942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-099-041A-3

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Alignment Scores:
Pred. No.: 9,31e-138 Length: 1620
Score: 1176.00 Matches: 226

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Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: 3 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-099-041A-3 (1-1620)

```
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
Db 937 AAGTTACAGAGTGTTCCTCAAGTGCCATTCACTATGTGACAAAGAAATGGAATATCT 996
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
Db 997 CTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGATCCTCTCAGCTCCAT 1056
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
Db 1057 GAAATAGTGGTTCCTCGAATCTCAAGTCCCTGCCAGCTCTCAAGACATGATTTT 1116
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
Db 1117 TTATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGTCTGGAATCAC 1176
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
Db 1177 AGTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCAT 1236
QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
Db 1237 CCATGCTCTTCAGCAATATATATCACTCTCACTGCAAGAACTCAGAACCTCTGCAG 1296
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValGlnLysLeu 144
Db 1297 CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACA 1356
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
Db 1357 GAAGCCTGCTTAACAGCTGCTAGATGCCCTTCTGTCAGGGACTGTGATCATGAAGAG 1416
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
Db 1417 GACTATGAATCTGTAGTACCAAGCTTACAGGACCTCAAAAGTCAGACATTTACTAGAC 1476
QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
Db 1477 ACTACTGACATCCAGGAGGAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAAC 1536
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
Db 1537 AAACAAATGGGTCTTCAGCCTTACCCGGAATACTTGTGTTTCTAGATCACCATCTTTA 1596
QY 225 AsnLeuLeuGlnAsnLysSerMet 232
Db 1597 AATTTACTCAAAATAAAGCATG 1620
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RESULT 4

US-09-245-281-3
; Sequence 3, Application US/09245281
; Patent No. 6369196
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/09/245,281
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: US 09/207,359
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: US 09/099,041
; EARLIER FILING DATE: 1998-06-17
; EARLIER APPLICATION NUMBER: US 09/019,942
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-245-281-3

Alignment Scores:

Prod. No.: 9.31e-138 Length: 1620
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: 3 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-245-281-3 (1-1620)

```
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
Db 937 AAGTTACAGAGTGTTCCTCAAGTGCCATTCACTATGTGACAAAGAAATGGAATATCT 996
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
Db 997 CTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGATCCTCTCAGCTCCAT 1056
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
Db 1057 GAAATAGTGGTTCCTCGAATCTCAAGTCCCTGCCAGCTCTCAAGACATGATTTT 1116
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
Db 1117 TTATCTAGAAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGTCTGGAATCAC 1176
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
Db 1177 AGTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTGATCACAAGACCAT 1236
QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
Db 1237 CCATGCTCTTCAGCAATATATATCACTCTCACTGCAAGAACTCAGAACCTCTGCAG 1296
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValGlnMetThr 144
Db 1297 CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACA 1356
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
Db 1357 GAAGCCTGCTTAACAGCTGCTAGATGCCCTTCTGTCAGGGACTGTGATCATGAAGAG 1416
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
Db 1417 GACTATGAATCTGTAGTACCAAGCTTACAGGACCTCAAAAGTCAGACATTTACTAGAC 1476
QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
Db 1477 ACTACTGACATCCAGGAGGAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAAC 1536
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
Db 1537 AAACAAATGGGTCTTCAGCCTTACCCGGAATACTTGTGTTTCTAGATCACCATCTTTA 1596
QY 225 AsnLeuLeuGlnAsnLysSerMet 232
Db 1597 AATTTACTCAAAATAAAGCATG 1620
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RESULT 5

US-09-207-359B-3
; Sequence 3, Application US/09207359B
; Patent No. 6469140
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

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/ FILE REFERENCE: 07334-112001
/ CURRENT APPLICATION NUMBER: US/09/207,359B
/ CURRENT FILING DATE: 1998-12-08
/ PRIOR APPLICATION NUMBER: US/09/099,041
/ PRIOR FILING DATE: 1998-06-17
/ PRIOR APPLICATION NUMBER: US/09/019,942
/ PRIOR FILING DATE: 1998-02-06
/ NUMBER OF SEQ ID NOS: 47
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 1620
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-207-359B-3

Alignment Scores:
Pred. No.: 9,31e-138 Length: 1620
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: Gaps: 0

US-09-771-161A-93 (1-232) x US-09-207-359B-3 (1-1620)

QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
DB 937 AAGTTACAGAGTGTTTCAAGTGCATTCACCTATGTGACAGAGAAATGGAATTAICT 996
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
DB 997 CTGAACATACCTGTAATCATGTCTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1056
QY 45 GluAsnSerGlySerProGlnThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
DB 1057 GAAATAGTGGTTCTCTGAACTTCAAGTCCCTGCCAGCTCTCAACACAATGATTTT 1116
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84
DB 1117 TTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCCTCTGGAAATCAC 1176
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
DB 1177 AGTTGGATAGCCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTATCACAAGCCATT 1236
QY 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
DB 1237 CCATGCTCTTCAGCAATAATAATCCACTCTCACTGCAGGAACTCAGAACGCTCTGCAG 1296
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
DB 1297 CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAATGACA 1356
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspLeuIleMetLysGlu 164
DB 1357 GAAGCTGCTTAAACAGTCCGTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAG 1416
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
DB 1417 GACTATGAATCTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAAATTACTAGAC 1476
QY 185 ThrThrAspIleGlnGluGluPheAlaLysValIleValGlnLysLysAspAsn 204
DB 1477 ACTACTGACATCAAGGAGAAGAAATTTGCCAAAGTTATATAGTACAAAATTTGAAGATAAC 1536
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
DB 1537 AACAAATGGTCTTCAGCCTTACCCGGAATATCTTGTGGTTCTAGATCACCATCTTTA 1596
QY 225 AsnLeuLeuGlnAsnLysSerMet 232
DB 1597 AATTTACTTCAAAATAAAGCATG 1620
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```
RESULT 6
US-09-340-620A-3
/ Sequence 3, Application US/09340620A
/ Patent No. 6482933
/ GENERAL INFORMATION:
/ APPLICANT: Bertin, John
/ TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
/ FILE REFERENCE: 07334-124001
/ CURRENT APPLICATION NUMBER: US/09/340,620A
/ CURRENT FILING DATE: 1999-06-28
/ PRIOR APPLICATION NUMBER: US/09/245,281
/ PRIOR FILING DATE: 1999-02-05
/ PRIOR APPLICATION NUMBER: US/09/207,359
/ PRIOR FILING DATE: 1998-12-08
/ PRIOR APPLICATION NUMBER: US/09/099,041
/ PRIOR FILING DATE: 1998-06-17
/ PRIOR APPLICATION NUMBER: US/09/019,942
/ PRIOR FILING DATE: 1998-02-06
/ NUMBER OF SEQ ID NOS: 71
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 1620
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-340-620A-3

Alignment Scores:
Pred. No.: 9,31e-138 Length: 1620
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: Gaps: 0

US-09-771-161A-93 (1-232) x US-09-340-620A-3 (1-1620)

QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
DB 937 AAGTTACAGAGTGTTTCAAGTGCATTCACCTATGTGACAGAGAAATGGAATTAICT 996
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
DB 997 CTGAACATACCTGTAATCATGTCTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1056
QY 45 GluAsnSerGlySerProGlnThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
DB 1057 GAAATAGTGGTTCTCTGAACTTCAAGTCCCTGCCAGCTCTCAACACAATGATTTT 1116
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84
DB 1117 TTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCCTCTGGAAATCAC 1176
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
DB 1177 AGTTGGATAGCCACCATTTCTGGATCTCAAGGGCTGCATTTCTGTATCACAAGCCATT 1236
QY 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
DB 1237 CCATGCTCTTCAGCAATAATAATCCACTCTCACTGCAGGAACTCAGAACGCTCTGCAG 1296
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
DB 1297 CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTGAACCAATGACA 1356
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspLeuIleMetLysGlu 164
DB 1357 GAAGCTGCTTAAACAGTCCGTAGATGCCCTTCTGTCCAGGACTTGATCATGAAGAG 1416
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
DB 1417 GACTATGAATCTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAAATTACTAGAC 1476
QY 185 ThrThrAspIleGlnGluGluPheAlaLysValIleValGlnLysLysAspAsn 204
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Db 1477 ACTACTGACATCCAAAGAGAGAAATTTGCCAAAGTTATAGTACAAAATTCAAAAGATAAC 1536
Qy 205 LysGlnMetGlyLeuGlnProTyrProGluLeuValSerArgSerProSerLeu 224
Db 1537 AAACAAATGGTCTTTCAGCCTTACCCGGAATACTTGTGGTTTCTAGATCACCATCTTTA 1596
Qy 225 AsnLeuLeuGlnAsnLysSerMet 232
Db 1597 AATTACTTCAAAATAAAGCATG 1620
RESULT 7
US-09-865-364-3
; Sequence 3, Application US/09865364
; Patent No. 6613521
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/865,364
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ-ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-865-364-3
Alignment Scores:
Pred. No.: 9,31e-138 Length: 1620
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: 4 Gaps: 0
US-09-771-161A-93 (1-232) x US-09-865-364-3 (1-1620)
Qy 5 GlnLeuGlnSerValSerSerAlaHisLeuCysAspLysLysMetGluLeuSer 24
Db 937 AAGTTACAGAGTGTTCAGTGCCATTTCACCTATGTGACAAAGAAATGGAATTATCT 996
Qy 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
Db 997 CTGAACATACCTGTAATCATGTGTCACAAAGAAATCATGTGATCCTCTCAGTCCAT 1056
Qy 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
Db 1057 GAAATAGTGGTCTCTCTGAACTTCAGTGCCCTGACGCTCTCTCAAGACATGATTT 1116
Qy 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
Db 1117 TTATCTAGAAAAGCTCAAGACTGTATTTATGAAGCTGCATCACTGCTCGGAAATCAC 1176
Qy 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
Db 1177 AGTTGGATAGCACCATTTCTGATCTCAAGGGCTGCATCTGTGATCAAGACCAT 1236
Qy 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
Db 1237 CCATGCTCTTCAGCAATAAATAATCCACTCTCACTGCAGAAACTCAGAACTGTCGAG 1296
Qy 125 ProGlyIleAlaGlnGlnThrPleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
Db 1297 CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAGACATTTGTGAACCAATGACA 1356

Qy 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
Db 1357 GAAGCCTGCCTTAACAGTCGCTAGATGCCCTTCTGTCACGGGACTTGATCATGAAGAG 1416
Qy 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
Db 1417 GACTATGAATCTGTAGTACCAAGCCTACAAGGACCTCAAAAGCTCAGACAAATTTACTAGAC 1476
Qy 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
Db 1477 ACTACTGACATCCAAAGGAGAATAATTGCCAAAGTTATAGTACAAAATTTGAAAGATAAC 1536
Qy 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu 224
Db 1537 AAACAAATGGTCTTTCAGCCTTACCCGGAATACTTGTGGTTTCTAGATCACCATCTTTA 1596
Qy 225 AsnLeuLeuGlnAsnLysSerMet 232
Db 1597 AATTACTTCAAAATAAAGCATG 1620

RESULT 8

US-09-019-942-2
; Sequence 2, Application US/09019942
; Patent No. 6033855
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/019,942
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ-ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 2.0b
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-019-942-2
Alignment Scores:
Pred. No.: 1,24e-137 Length: 1620
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: 3 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-019-942-2 (1-1931)

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QY      5  GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24
      :::|
Db     1150  AAGTTACAGAGTGTTTCAAGTGCATTCACCTATGTGACAAGAGAAAATGGAATTATCT 1209
      |
QY     25  LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
      |
Db     1210  CTGAACATACCTGTAATCATGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1269
      |
QY     45  GluAsnSerGlySerProGlnThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
      |
Db     1270  GAAATAGTGGTTCCTGAACTTCAAGGTCCTGCCAGCTCCTCAAGACAATGATTTT 1329
      |
QY     65  LeuSerArgGlyAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
      |
Db     1330  TTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGCTCGAATAC 1389
      |
QY     85  SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
      |
Db     1390  AGTTGGATAGACACCATTTCTGATCTCAAGGCTGCATTTCTGATCACAAGACCATT 1449
      |
QY     105  ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
      |
Db     1450  CCATGCTCTTCAGCAATAATAATCCACTCAACTGCAGGAACTCAGAACGTCTGCAG 1509
      |
QY     125  ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
      |
Db     1510  CCTGGTATAGCCAGAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACA 1569
      |
QY     145  GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
      |
Db     1570  GAAGCCTGCTTAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAAGAG 1629
      |
QY     165  AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
      |
Db     1630  GACTATGAATCTGTAGTACCAAGCCTACAGGACCTCAAAAGTCAAGACAATTTACTAGAC 1689
      |
QY     185  ThrThrAspIleGlnGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
      |
Db     1690  ACTACTGACATCCAAAGGAAGAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAAC 1749
      |
QY     205  LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
      |
Db     1750  AAACAAATGGCTTCCAGCCTTACCCGGAATACTTGTGGTTCTTAGATCACAATCTTTA 1809
      |
QY     225  AsnLeuLeuGlnAsnLysSerMet 232
      |
Db     1810  AATTTACTTCAAAATAAAAGCATG 1833

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RESULT 9

US-09-099-041A-1
; Sequence 1, Application US/09099041A
; Patent No. 6340576

GENERAL INFORMATION:

; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/09/099,041A
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214) ... (1833)

Alignment Scores:

Pred. No.: 1,24e-137 Length: 1931
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: Gaps: 0

US-09-771-161A-93 (1-232) x US-09-099-041A-1 (1-1931)

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QY      5  GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24
      :::|
Db     1150  AAGTTACAGAGTGTTTCAAGTGCATTCACCTATGTGACAAGAGAAAATGGAATTATCT 1209
      |
QY     25  LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
      |
Db     1210  CTGAACATACCTGTAATCATGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1269
      |
QY     45  GluAsnSerGlySerProGlnThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
      |
Db     1270  GAAATAGTGGTTCCTGAACTTCAAGGTCCTGCCAGCTCCTCAAGACAATGATTTT 1329
      |
QY     65  LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
      |
Db     1330  TTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGCTCGAATAC 1389
      |
QY     85  SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
      |
Db     1390  AGTTGGATAGACACCATTTCTGATCTCAAGGCTGCATTTCTGATCACAAGACCATT 1449
      |
QY     105  ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
      |
Db     1450  CCATGCTCTTCAGCAATAATAATCCACTCAACTGCAGGAACTCAGAACGTCTGCAG 1509
      |
QY     125  ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
      |
Db     1510  CCTGGTATAGCCAGAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACA 1569
      |
QY     145  GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
      |
Db     1570  GAAGCCTGCTTAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAAGAG 1629
      |
QY     165  AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
      |
Db     1630  GACTATGAATCTGTAGTACCAAGCCTACAGGACCTCAAAAGTCAAGACAATTTACTAGAC 1689
      |
QY     185  ThrThrAspIleGlnGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
      |
Db     1690  ACTACTGACATCCAAAGGAAGAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAAC 1749
      |
QY     205  LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
      |
Db     1750  AAACAAATGGGCTTCCAGCCTTACCCGGAATACTTGTGGTTCTTAGATCACAATCTTTA 1809
      |
QY     225  AsnLeuLeuGlnAsnLysSerMet 232
      |
Db     1810  AATTTACTTCAAAATAAAAGCATG 1833

```

RESULT 10

US-09-245-281-1

; Sequence 1, Application US/09245281
; Patent No. 6369196

GENERAL INFORMATION:

; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/09/245,281
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: US 09/207,359
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: US 09/099,041

EARLIER FILING DATE: 1998-06-17
EARLIER APPLICATION NUMBER: US 09/019,942
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1931
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (214) ... (1833)
US-09-245-281-1

Alignment Scores:
Pred. No.: 1-24e-137 Length: 1931
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: 3 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-245-281-1 (1-1931)

```
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
Db 1150 AAGTTACAGAGTGTTCACAGTGCCATTCACCTATGTGACAAAGAAATGGAATATCT 1209
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
Db 1210 CTGAACATACCTGTAATCATGTGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1269
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
Db 1270 GAAATAGTGGTCTCTGAAATCTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTT 1329
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
Db 1330 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGTGCATCACTGCTCGAATAC 1389
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
Db 1390 AGTTGGGATAGCACCATTCTTGATCTCAAGGGCTGCATTCTGTGATCAACAAGACCATT 1449
QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
Db 1450 CCATGCTCTTCAGCAATATAAATCCACTCTCAACTGCAGAAACTCAGAACCTCTGCAG 1509
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
Db 1510 CCTGGTATAGCCAGCAGTGTGATCCAGACAAAGGGAGACATTGTGAACCAATGACA 1569
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
Db 1570 GAAGCCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGACCTTGATCATGAAGAG 1629
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
Db 1630 GACTATGAACCTGTGTAGTACCAAGCCTTACAGGACCTCAAAAGTCCAGACAATTAC 1689
QY 185 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
Db 1690 ACTACTGACATCCAGGAGAGAAATTTGCCAAGTTATAGTACAAAATTTGAAGATAC 1749
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
Db 1750 AAACAAATGGTCTTCAGCCTTACCCGAAATATCTGTGGTCTTAGATCACCATCTTTA 1809
QY 225 AsnLeuLeuGlnAsnLysSerMet 232
Db 1810 AATTACTTCAAAATAAAGCATG 1833
```

RESULT 11

US-09-470-271-2
Sequence 2, Application US/09470271
Patent No. 6410689
GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
TITLE OF INVENTION: DOMAIN POLYPEPTIDES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/470,271
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/019,942
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Meikiejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/068001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1931 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-470-271-2

Alignment Scores:
Pred. No.: 1-24e-137 Length: 1931
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: 4 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-470-271-2 (1-1931)

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QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
Db 1150 AAGTTACAGAGTGTTCACAGTGCCATTCACCTATGTGACAAAGAAATGGAATATCT 1209
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
Db 1210 CTGAACATACCTGTAATCATGTGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1269
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
Db 1270 GAAATAGTGGTCTCTGAAATCTCAAGTCCCTGCCAGCTCCTCAAGACAATGATTTT 1329
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
Db 1330 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGTGCATCACTGCTCGAATAC 1389
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
Db 1390 AGTTGGGATAGCACCATTCTTGATCTCAAGGGCTGCATTCTGTGATCAACAAGACCATT 1449
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QY 105 ProCysSerSerAlaIleIleLeuProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
 DB 1450 CCATGCTCTTCAGCAATAATAATCACTCTCAACTGCAGGAACTCAGAACGTCGCGAG 1509
 QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
 DB 1510 CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATGTGTGAACCAATGACA 1569
 QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
 DB 1570 GAAGCCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCAGGAGCTTGTATCATGAAGAG 1629
 QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
 DB 1630 GACTATGAATGTGTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAATTTACTAGAC 1689
 QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
 DB 1690 ACTACTGACATCCAGAGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAAC 1749
 QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
 DB 1750 AAACAAATGGTCTTCAGCCTTACCGGAAATACTTGTGTTTCTAGATCACCATCTTTA 1809
 QY 225 AsnLeuLeuGlnAsnLysSerMet 232
 DB 1810 AATTTACTTCAAAATAAAAGCATG 1833

RESULT 12

US-09-207-359B-1
 ; Sequence 1, Application US/09207359B
 ; Patent No. 6469140
 ; GENERAL INFORMATION:
 ; APPLICANT: Bertin, John
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
 ; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
 ; FILE REFERENCE: 07334-112001
 ; CURRENT APPLICATION NUMBER: US/09/207,359B
 ; CURRENT FILING DATE: 1998-12-08
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR FILING DATE: 1998-02-06
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1931
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (214)...(1833)
 US-09-207-359B-1

Alignment Scores:
 Pred. No.: 1,24e-137 Length: 1931
 Score: 1176.00 Matches: 226
 Percent Similarity: 99.56% Conservative: 1
 Best Local Similarity: 99.12% Mismatches: 1
 Query Match: 97.51% Indels: 0
 DB: 4 Gaps: 0

US-09-771-161a-93 (1-232) x US-09-207-359B-1 (1-1931)

QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
 DB 1150 AAGTTACAGAGTGTTCAGTGCCATTCACCTATGTGACAGAGAAATTTGAATATCT 1209
 QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
 DB 1210 CTGAACATACCTGTAATATCATGGTCCACAGAGGAATCATGTGATCTCTACGCTCAT 1269
 QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64

DB 1270 GAAATAAGTGGTTCCTGAAACTTCAGGTCCTCGCAGCTCTCAAGCAATGATTTT 1329
 QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84
 DB 1330 TTATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGCTCTCGGAAATCAC 1389
 QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaPheCysAspHisLysThrThr 104
 DB 1390 AGTTGGGATACACCATTTCTGGATCTCAAGGGCTGCAITTCGTGATCAAGACCCATT 1449
 QY 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
 DB 1450 CCATGCTCTTCAGCAATAATAATCCACTCTCACTGCAGGAACTCAGAACGTCGCGAG 1509
 QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
 DB 1510 CCTGATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACA 1569
 QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
 DB 1570 GAAGCCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCAGGAGCTTGTATCATGAAGAG 1629
 QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
 DB 1630 GACTATGAATGTGTAGTACCAAGCCTACAAAGACCTCAAAAGTCAGACAATTTACTAGAC 1689
 QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
 DB 1690 ACTACTGACATCCAGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAAC 1749
 QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
 DB 1750 AAACAAATGGTCTTCAGCCTTACCGGAAATACTTGTGTTTCTAGATCACCATCTTTA 1809
 QY 225 AsnLeuLeuGlnAsnLysSerMet 232
 DB 1810 AATTTACTTCAAAATAAAAGCATG 1833

RESULT 13

US-09-340-620A-1
 ; Sequence 1, Application US/09340620A
 ; Patent No. 6482933
 ; GENERAL INFORMATION:
 ; APPLICANT: Bertin, John
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
 ; FILE REFERENCE: 07334-124001
 ; CURRENT APPLICATION NUMBER: US/09/340,620A
 ; CURRENT FILING DATE: 1999-06-28
 ; PRIOR FILING DATE: 1999-06-28
 ; PRIOR FILING DATE: 1999-02-05
 ; PRIOR FILING DATE: 1999-02-05
 ; PRIOR FILING DATE: 1998-12-08
 ; PRIOR FILING DATE: 1998-12-08
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR FILING DATE: 1998-02-06
 ; NUMBER OF SEQ ID NOS: 71
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1931
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (214)...(1833)
 US-09-340-620A-1

Alignment Scores:
 Pred. No.: 1,24e-137 Length: 1931
 Score: 1176.00 Matches: 226
 Percent Similarity: 99.56% Conservative: 1
 Best Local Similarity: 99.12% Mismatches: 1

Query Match: 97.51% Indels: 0
DB: 4 Gaps: 0
US-09-771-161a-93 (1-232) x US-09-340-620A-1 (1-1931)
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24
DB 1150 AAGTTACAGAGTGTTCCTCAAGTGCCTCACTATGTGACAGAGAAAGAAATGGAATATCT 1209
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
DB 1210 CTGAACATACCTGTAATCATGTGTCACAGAGAAATCATGTGATCTCTCAGCTCCAT 1269
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPhe 64
DB 1270 GAAATAGTGGTCTCTCGAACTTCAAGTCCCTCCAGCAATGATTTT 1329
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
DB 1330 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGCTCGAAATCAC 1389
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
DB 1390 AGTTGGATAGCACCATTCTGGATCTCAAGGGCTGCATCTGTGATCAAGACCATT 1449
QY 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
DB 1450 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACTGTCGAG 1509
QY 125 ProGlyIleAlaGlnTrpIleGlnSerLysArgGluAspLysValAsnGlnMetThr 144
DB 1510 CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACA 1569
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspLeuLeuMetLysGlu 164
DB 1570 GAAGCTGCTTAACAGTGCCTAGATGCCCTTCTGTCAGGACTTGTATGAAAGAG 1629
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
DB 1630 GACTATGAACCTTGTAGTACCAAGCTTACCAAGCTCAAAAGTCAAGCAATTTACTAGAC 1689
QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
DB 1690 ACTACTGACATCCAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAAC 1749
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
DB 1750 AAACAAATGGTCTTCCAGCTTACCCGAAATACCTTGTGGTTTCTAGATCACCATTCTTTA 1809
QY 225 AsnLeuLeuGlnAsnLysSerMet 232
DB 1810 AATTACTTCAAAATAAAGCATG 1833

RESULT 14

US-09-865-364-1
; Sequence 1, Application US/09865364
; Patent No. 6613521
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/865,364
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1

; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)...(1833)
US-09-865-364-1
Alignment Scores:
Pred. No.: 1-246-137 Length: 1931
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: 4 Gaps: 0

US-09-771-161a-93 (1-232) x US-09-865-364-1 (1-1931)

QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24
DB 1150 AAGTTACAGAGTGTTCCTCAAGTGCCTCACTATGTGACAGAGAAAGAAATGGAATATCT 1209
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
DB 1210 CTGAACATACCTGTAATCATGTGTCACAGAGAAATCATGTGATCTCTCAGCTCCAT 1269
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAspPhe 64
DB 1270 GAAATAGTGGTCTCTCGAACTTCAAGTCCCTCCAGCTCTCTCAAGCAATGATTTT 1329
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
DB 1330 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGCTCGAAATCAC 1389
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
DB 1390 AGTTGGATAGCACCATTCTGGATCTCAAGGGCTGCATCTGTGATCAAGACCATT 1449
QY 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
DB 1450 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACTGTCGAG 1509
QY 125 ProGlyIleAlaGlnTrpIleGlnSerLysArgGluAspLysValAsnGlnMetThr 144
DB 1510 CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACA 1569
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuSerArgAspLeuLeuMetLysGlu 164
DB 1570 GAAGCTGCTTAACAGTGCCTAGATGCCCTTCTGTCAGGACTTGTATGAAAGAG 1629
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
DB 1630 GACTATGAACCTTGTAGTACCAAGCTTACCAAGCTCAAAAGTCAAGCAATTTACTAGAC 1689
QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
DB 1690 ACTACTGACATCCAGGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAAC 1749
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
DB 1750 AAACAAATGGTCTTCCAGCTTACCCGAAATACCTTGTGGTTTCTAGATCACCATTCTTTA 1809
QY 225 AsnLeuLeuGlnAsnLysSerMet 232
DB 1810 AATTACTTCAAAATAAAGCATG 1833

RESULT 15

US-09-748-537-2
; Sequence 2, Application US/09748537
; Patent No. 6680167
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Chao, Moses V.

;; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILIE AND USES THERE

;; FILE REFERENCE: 07334-316001
;; CURRENT APPLICATION NUMBER: US/09/748,537
;; CURRENT FILING DATE: 2000-12-26
;; PRIOR APPLICATION NUMBER: US 09/099,041
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: US 09/019,942
;; PRIOR FILING DATE: 1998-02-06
;; NUMBER OF SEQ ID NOS: 14
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2
;; LENGTH: 1931
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-748-537-2

Alignment Scores: 1.24e-137 Length: 1931
Pred. No.: 1176.00 Matches: 226
Score: 1176.00
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: 4 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-748-537-2 (1-1931)

QY 5 GlnLeuGlnSerValSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24
Db 1150 AAGTTACAGAGTGTTCACGTGTCACCTATGTGACAGAGAAATGGAATATCT 1209
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
Db 1210 CTGAACATACCTGTAAATCATGTGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1269
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
Db 1270 GAAATAGTGGTTCCTCTGAACTTCAGGTCCCTGCCAGCTCCTCAGACAAATGATTT 1329
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84
Db 1330 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGCTCGGAAATCAC 1389
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
Db 1390 AGTTGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTCGTGATCAAGACCAAT 1449
QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
Db 1450 CCATGCTCTTCAGCAATAATAATCCACTCTCAACTGCAGGAAACTCAGAACGCTTCGAG 1509
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
Db 1510 CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTTGTAACCAAAATGACA 1569
QY 145 GluAlaCysLeuLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
Db 1570 GAAGCCTGCCCTTAACAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAGAG 1629
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
Db 1630 GACTATGAACCTTTAGTACCAAGCCTACAGGACCTCAAAAGTCAGACAAATTAAGAC 1689
QY 185 ThrThrAspIleGlnGlnGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
Db 1690 ACTACTGACATCCAGAGGAGAGAAATTTGCCAAAGTTATAGTACAAAATTTGAAGATAAC 1749
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
Db 1750 AAACAAATGGGTCTTCAGCCTTACCGGAATATACTTTGTGGTTTCTAGATCACCATCTTTA 1809
QY 225 AsnLeuLeuGlnAsnLysSerMet 232
Db 1810 AATTACTTCAAAATAAAAGCATG 1833

Search completed: February 1, 2005, 01:26:56
Job time : 115 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 31, 2005, 23:09:56 ; Search time 573 Seconds
(without alignments)
2326.433 Million cell updates/sec

Title: US-09-771-161A-93

Perfect score: 1206

Sequence: 1 MYSLQLQSSVAIHLCDKKK.....PEILVVSFSLNLLQKSM 232

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100
-MINLEN=2000000000 -USER=US09771161.OCGN 1 1 480 @runat_28012005_103500_31
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSFBLOCK=100
-LONGLOG -DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq*
5: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq*
6: /cgn2_6/prodata/1/pubpna/PCTUS_PUBCOMB.seq*
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9: /cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq*
10: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq*
11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq*
12: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq*
13: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq*
14: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq*
15: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq*
16: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq*
17: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq*
18: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq*
19: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq*
20: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq*
21: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1206	100.0	1669	9	US-09-771-161A-2	Sequence 2, Appli
2	1182	98.0	1623	15	US-10-172-118-957	Sequence 957, App
3	1182	98.0	1623	16	US-10-342-887-957	Sequence 13, Appl
4	1182	98.0	2501	10	US-09-981-397A-13	Sequence 35, Appl
5	1182	98.0	2501	18	US-10-825-282-35	Sequence 173, App
6	1182	98.0	2709	9	US-09-925-301-173	Sequence 3, Appli
7	1176	97.5	1620	9	US-09-728-721-3	Sequence 3, Appli
8	1176	97.5	1620	13	US-10-105-931-3	Sequence 3, Appli
9	1176	97.5	1620	13	US-10-118-984-3	Sequence 3, Appli
10	1176	97.5	1620	15	US-10-295-981-3	Sequence 1, Appli
11	1176	97.5	1931	9	US-09-748-537-2	Sequence 1, Appli
12	1176	97.5	1931	9	US-09-728-721-1	Sequence 2, Appli
13	1176	97.5	1931	13	US-10-133-780-2	Sequence 1, Appli
14	1176	97.5	1931	13	US-10-105-931-1	Sequence 1, Appli
15	1176	97.5	1931	13	US-10-118-984-1	Sequence 1, Appli
16	1176	97.5	1931	15	US-10-295-981-1	Sequence 1, Appli
17	1165	96.6	1060	16	US-10-641-643-684	Sequence 684, App
18	650	53.9	491	10	US-09-918-995-20565	Sequence 20565, A
19	125	10.4	1400	9	US-09-728-721-40	Sequence 40, Appl
20	125	10.4	1400	13	US-10-118-984-40	Sequence 40, Appl
21	125	10.4	1400	15	US-10-006-883A-96	Sequence 96, Appl
22	125	10.4	1400	15	US-10-295-981-40	Sequence 40, Appl
23	125	10.4	3382	9	US-09-728-721-7	Sequence 7, Appli
24	125	10.4	3382	13	US-10-105-931-7	Sequence 7, Appli
25	125	10.4	3382	13	US-10-118-984-7	Sequence 7, Appli
26	125	10.4	3382	15	US-10-295-981-7	Sequence 2, Appli
27	125	10.4	4093	15	US-10-401-194-2	Sequence 38, Appl
28	125	10.4	4302	9	US-09-728-721-38	Sequence 38, Appl
29	125	10.4	4302	13	US-10-118-984-38	Sequence 95, Appl
30	125	10.4	4302	15	US-10-006-883A-95	Sequence 38, Appl
31	125	10.4	4302	15	US-10-295-981-38	Sequence 3, Appli
32	125	10.4	4390	15	US-10-006-883A-3	Sequence 3, Appli
33	125	10.4	4415	14	US-10-013-477-3	Sequence 11, Appl
34	125	10.4	4610	15	US-10-006-883A-11	Sequence 9, Appli
35	122.5	10.2	2859	9	US-09-728-721-9	Sequence 9, Appli
36	122.5	10.2	2859	13	US-10-105-931-9	Sequence 9, Appli
37	122.5	10.2	2859	13	US-10-118-984-9	Sequence 9, Appli
38	122.5	10.2	2859	15	US-10-295-981-9	Sequence 10, Appl
39	122.5	10.2	3789	14	US-10-013-477-10	Sequence 2086, Ap
40	122.5	10.2	3693	15	US-10-106-698-2086	Sequence 13799, A
41	114	9.5	60	10	US-09-908-975-13799	Sequence 4, Appli
42	104.5	8.7	626	9	US-09-748-537-4	Sequence 4, Appli
43	104.5	8.7	626	13	US-10-133-780-4	Sequence 27, Appl
44	104.5	8.7	1470	9	US-09-728-721-27	Sequence 27, Appl
45	104.5	8.7	1470	13	US-10-105-931-27	

ALIGNMENTS

RESULT 1
US-09-771-161A-2
; Sequence 2, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1669
; TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: -

LOCATION: (1)..(1669)

OTHER INFORMATION: "n" can be any nucleotide 'a', 'c', 'g' or 't'

US-09-771-161A-2

Alignment Scores:

Pred. No.: 9, 4e-137 Length: 1669
Score: 1206.00 Matches: 232
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-771-161A-2 (1-1669)

QY 1 MetTyrSerLeuGlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLys 20
DB 320 ATGTATTTCATTACAGTTACAGAGTGTTCAGGTGCCATTCACCTATGTGACAGAGAA 379
QY 21 MetGluLeuSerLeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySer 40
DB 380 ATGGAATATCTCTGAACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCC 439
QY 41 SerGlnLeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGln 60
DB 440 TCTCAGCTCCATGAAATAGTGGTTCTCTGAAACTTCAAGGTCTCCAGCTCCCTCAA 499
QY 61 AspAsnAspPheLeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCys 80
DB 500 GACAATGATTTTATCTAGAAAAGCTCAAGACTGTATTTATTAAGAGCTGCATCACTGT 559
QY 81 ProGlyAsnHisSerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAsp 100
DB 560 CCTGGAAATCACAGTTGGATAGACCACTTCTGGATCTCAAGGGCTGCATTCTCTGAT 619
QY 101 HisLysThrThrProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSer 120
DB 620 CACAAGACCCTCCATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCAGGAACTCA 679
QY 121 GluArgLeuGlnProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleVal 140
DB 680 GAAGCTCTGAGCCTGTGTATAGCCAGCAGTGTATCCAGAGCAAAAGGGAGACATTGTG 739
QY 141 AsnGlnMetThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeu 160
DB 740 AACCAATGACAGAGCCTGCTTAAACAGTGCCTAGATGCCCTTCTGTCCAGGACTTG 799
QY 161 IleMetLysGluAspTyrGluLeuValSerThrIleProThrArgThrSerLysValArg 180
DB 800 ATCATGAAAGAGGACTATGAACCTTTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGA 859
QY 181 GlnLeuLeuAspThrThrAspIleGlnGluGluPheAlaLysValIleValGlnLys 200
DB 860 CAATTACTAGACACTACTGACATCCAGGAGAGAAATTTGCCAAGTTATAGTACAAAA 919
QY 201 LeuLysAspAsnLysGlnMetGlyLeuGlnProTyrProGluLeuValValSerArg 220
DB 920 TTGAAAGATAACAAACAAATGGGTCTTCAGCCTTTACCCGGAATATCTTGTGGTTCTAGA 979
QY 221 SerProSerLeuAsnLeuGlnAsnLysSerMet 232
DB 980 TCACCATCTTTAAATTTACTTCAAAATATAAGCATG 1015

RESULT 2

US-10-172-118-957

Sequence 957, Application US/10172118

Publication No. US20030224374A1

GENERAL INFORMATION:

APPLICANT: Dai, Hongyue

APPLICANT: He, Yudong

APPLICANT: Linsley, Peter

APPLICANT: Mao, Mao
APPLICANT: Roberts, Chris
APPLICANT: Van 't Veer, Laura
APPLICANT: Van de Vijver, Marc
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-175-999
CURRENT APPLICATION NUMBER: US/10/172,118
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 957
LENGTH: 1623
TYPE: DNA
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NM_003821
DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-957

Alignment Scores:

Pred. No.: 7, 73e-134 Length: 1623
Score: 1182.00 Matches: 227
Percent Similarity: 100.00% Conservatives: 1
Best Local Similarity: 99.56% Mismatches: 0
Query Match: 98.01% Indels: 0
DB: 15 Gaps: 0

US-09-771-161A-93 (1-232) x US-10-172-118-957 (1-1623)

QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
DB 937 AAGTTACAGAGTGTTCAGGTGCCATTCACCTATGTGACAGAGAAATGGAATTATCT 996
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeuHis 44
DB 997 CTGACATACCTGTAAATCATGTGTCACAGAGGAATCATGTGGATCTCTCAGCTCCAT 1056
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
DB 1057 GAAATATAGTGGTCTTCCTGAAACTTCAAGGTCCCTCCAGCTCTCTCAAGACAATGATTTT 1116
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
DB 1117 TTATCTAGAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGCTCGAAATCAC 1176
QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
DB 1177 AGTTGGGACAGCACCATTCTCGATCTCAAAGGGCTGCATTTCTGTGATCACAAGACCCT 1236
QY 105 ProCysSerSerAlaIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
DB 1237 CCATGCTCTTCAGCAATAATAAATCCATCTCCTCACTGAGGAACTCAGACGCTCGCAG 1296
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
DB 1297 CTTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGCATTTGTGAACCAATGACA 1356
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
DB 1357 GAAGCCTGCTTAAACAGTGCCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGAG 1416
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
DB 1417 GACTATGAATCTGTGTAGTACCAAGCCTCAAGGACCTCAAAAGTCAGACAATTTACTAGAC 1476
QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
DB 1477 ACTACTGACATCCAGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAGATAAC 1536
QY 205 LysGlnMetGlyLeuGlnProTyrProGluLeuValValSerArgSerProSerLeu 224

Db 1537 AACAAATGGGTCTTCAGCCTTACCCGGAATACTCTGGTTTCTAGATCACCATCTTTA 1596

Qy 225 AsnLeuLeuGlnAsnLysSerMet 232
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Db 1597 AATTTACTCTCAAAATAAAAGCATG 1620

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RESULT 3
US-10-342-887-957
; Sequence 957, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernard, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 957
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-957

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Alignment Scores:		
Pred. No.:		1623
Score:	7.73e-134	
Percent Similarity:	1182.00	Matches: 1227
Best Local Similarity:	100.00%	Conservative: 1
Query Match:	99.56%	Mismatches: 0
DB:	98.01%	Indels: 0
	16	Gaps: 0
US-09-771-161A-93 (1-232)	x US-10-342-887-957 (1-1623)	

Db 1401 AGTTGGGATAGCACCATTCTGGTTCTCAAGGGCTGCATTCTGTGATCACAAGACCACT 1460
Qy 105 ProCysSerSerAlaIleIleLeuProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
Db 1461 CCATGCTCTTCAGCAATAATAATCCACTCTCACTGCAGGAACTCAGACGCTCTGCAG 1520
Qy 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
Db 1521 CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTGTGAACCAATGACA 1580
Qy 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspIleMetLysGlu 164
Db 1581 GAAGCCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGAG 1640
Qy 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
Db 1641 GACTATGAATCTGTATGATACCAAGCTTACAGGACCTCAAAAGTCAGACAATTACTAGAC 1700
Qy 185 ThrThrAspIleGlnGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
Db 1701 ACTACTGACATCCAGGAGAGAATTTGCCAAAGTTATAGTACAAAAATTGAAGATAAC 1760
Qy 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
Db 1761 AAACAAATGGGCTCTCAGCCCTTACCCGGAATACTTGTGGTTCTAGATCACAATCTTTA 1820
Qy 225 AsnLeuLeuGlnAsnLysSerMet 232
Db 1821 AATTACTTCAAAATAAAGCATG 1844

RESULT 5

US-10-825-282-35
; Sequence 35, Application US/10825282
; Publication No. US20040224389A1
; GENERAL INFORMATION:
; APPLICANT: 3921-1-1-1
; TITLE OF INVENTION: VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND
; FILE REFERENCE: 3921-1-1-1
; CURRENT FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/456,357
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: 60/134,416
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 09/087,195
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 08/378,507
; PRIOR FILING DATE: 1995-01-26
; PRIOR APPLICATION NUMBER: 08/250,478
; PRIOR FILING DATE: 1994-05-27
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 2501
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (225)..(1847)
US-10-825-282-35

Alignment Scores:
Pred. No.: 1,466-133 Length: 2501
Score: 1182.00 Matches: 227
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.56% Mismatches: 0
Query Match: 98.01% Indels: 0
DB: 18 Gaps: 0

US-09-771-161A-93 (1-232) x US-10-825-282-35 (1-2501)

Qy 5 GlnLeuGlnSerValSerSerAlaIleIleHisLeuCysAspLysLysLysMetGluLeuSer 24
Db 1161 AAGTTACAGAGTGTTCAGTGCCATTACCTAATGTGACAAAGAAATATGGAATATCT 1220
Qy 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
Db 1221 CTGAACATACCTGTAAATCATGGTCCACAAGAGAAATCATGTGGATCCTCTCAGCTCAT 1280
Qy 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
Db 1281 GAAATAATAGTGGTTCTCTCGAAACTTCAAGGTCCCTGCCAGCTCTCTCAAGCAATATGATTTT 1340
Qy 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84
Db 1341 TTATCTAGAAAGCTCAAGACTGTATTTTATGAAGCTGCATCACTGTCTCTGGAATATCAC 1400
Qy 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThrThr 104
Db 1401 AGTTGGGATAGCACCATTCTGGTTCTCAAGGGCTGCATTCTGTGATCACAAGACCACT 1460
Qy 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
Db 1461 CCATGCTCTTCCAGCAATAATAATCCACTCTCAACTGCAGGAACTCAGAACGCTCTGCAG 1520
Qy 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
Db 1521 CTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTGTGAACCAATGACA 1580
Qy 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
Db 1581 GAAGCCTGCTTAAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGAG 1640
Qy 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
Db 1641 GACTATGAATCTGTATGATACCAAGCTTACAGGACCTCAAAAGTCAGACAATTACTAGAC 1700
Qy 185 ThrThrAspIleGlnGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
Db 1701 ACTACTGACATCCAGGAGAGAATTTGCCAAAGTTATAGTACAAAAATTGAAGATAAC 1760
Qy 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
Db 1761 AAACAAATGGGCTCTCAGCCCTTACCCGGAATACTTGTGGTTCTAGATCACAATCTTTA 1820
Qy 225 AsnLeuLeuGlnAsnLysSerMet 232
Db 1821 AATTACTTCAAAATAAAGCATG 1844
RESULT 6
US-09-925-301-173
; Sequence 173, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 173
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2595)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature

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; LOCATION: (2622)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc.feature
; LOCATION: (2659)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc.feature
; LOCATION: (2670)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-173

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Alignment Scores:		
Pred. No.:	1.64e-133	Length: 2709
Score:	1182.00	Matches: 227
Percent Similarity:	100.00%	Conservative: 1
Best Local Similarity:	99.56%	Mismatches: 0
Query Match:	98.01%	Indels: 0
DB:	9	Gaps: 0

US-09-771-161A-93 (1-232) x US-09-925-301-173 (1-2709)

Qy	5	GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer	24
Db	1203	AAAGTACAGAGTGTTCCTCAAGTGCATTCACCTATGTGACAAGAAGAAAATGGAAATATCT	1262
Qy	25	LeuAsnIleProValIleHisGlyProGlnGluLeuSerCysGlySerSerGlnLeuHis	44
Db	1263	CTGAACATACCTGTAAATCATGTGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCAT	1322
Qy	45	GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe	64
Db	1323	GAANAATAGTGGTCTCTCTGAACTTCAAGGTCTCTGCCAGCTCTCTCAAGACAATGATTTT	1382
Qy	65	LeuSerArgLysAlaGlnAspCysIlePheMetLysLeuHisCysCysProGlyAsnHis	84
Db	1383	TTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACGTCTCGTGGAAATCAC	1442
Qy	85	SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr	104
Db	1443	AGTGTGGAYAGCACCATTTCTCGAATCTCAAGGGCTGCATTCTGTGATCAACAAGACCCT	1502
Qy	105	ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGluValAsnSerGluArgLeuGln	124
Db	1503	CCATGTCTTTCAGCAATATTAATTCCTCTCAACTGTCAGAAACTCAGAACCTGTGCAG	1562
Qy	125	ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr	144
Db	1563	CCTGGTATAGCCAGCAGCTGATCCAGAGCAAAAGGGAAGACATTTGTGAACCAATGACA	1622
Qy	145	GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspIleMetLysGlu	164
Db	1623	GAAGCCTGCCTTTAACAGTCGCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAGAG	1682
Qy	165	AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp	184
Db	1683	GACTATGAACCTGTGTAGTACCAAGCCTTACAAAGACCTCAAAAGTCAGACAAATTTACTAGAC	1742
Qy	185	ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn	204
Db	1743	ACTACTGACATCCAGGAGAGAAGATTTGCCAAGTTATAGTACAAAATTTGAAGATTAAC	1802
Qy	205	LysGlnMetGlyLeuGlnProTyrProGluIleLeuValSerArgSerProSerLeu	224
Db	1803	AAACAAATGGTCTTTCAGCCTTACC CGGAAATACTTGTGGTTTCTAGATCACCATCTTTA	1862
Qy	225	AsnLeuLeuGlnAsnLysSerMet	232
Db	1863	AAATTACTTCCAAATAAAAGCATG	1886

RESULT 7

US-09-728-721-3
; Sequence 3, Application US/09728721
; Patent No. US20020061845A1
; GENERAL INFORMATION:

Db 1237 CCATGCTCTTACGCAATAATAAATCCACTCTCACTCAGGAACTCAGAACGCTGTCAG 1296
Qy 125 ProGlyIleAlaGlnGlnTrpIleGlnSerIleArgGluAspIleValAsnGlnMetThr 144
Db 1297 CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGGAAGACATTGTAACCAATGACA 1356
Qy 145 GluAlaCysIleuAsnGlnSerLeuAspAlaLeuIleuSerArgAspLeuIleMetLysGlu 164
Db 1357 GAAGCCTGCCTTAACCAAGTCGTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGAG 1416
Qy 165 AspTyrGluLeuValSerThrIleValProGlyIleValSerIleValArgGlnLeuLeuAsp 184
Db 1417 GACTATGAACCTTGTATGACCAAGCCTCAAGGACCTCAAAAGTCAGACAAATTAAGAC 1476
Qy 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
Db 1477 ACTACTGACATCCAGAGGAAGATTTGCCAAGTTATAGTACAAAATTTGAAGATTAAC 1536
Qy 205 LysGlnMetGlyLeuGlnProTyrProGlyIleValSerArgSerProSerLeu 224
Db 1537 AAACAAATGGTCTTTCAGCCTTACCCGGAATACTTGTGTCTTAGATCACCATTCTTA 1596
Qy 225 AsnLeuLeuGlnAsnLysSerMet 232
Db 1597 AATTTACTTCAAAATAAAAGCATG 1620

RESULT 10

US-10-295-981-3
; Sequence 3, Application US/10295981
; Publication No: US20030120055A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/10/295,981
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US/09/245,281
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US/09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US/09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US/09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-981-3

Alignment Scores:
Pred. No.: 4,17e-133 Length: 1620
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: 15 Gaps: 0

US-09-771-161a-93 (1-232) x US-10-295-981-3 (1-1620)

Qy 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
Db 937 AAGTTACAGTAGTGTTCAGTGCCATTCACCTATGTGACAAAGGAAGAAATGGAATTATCT 996
Qy 25 LeuAsnIleProValAsnHisGlyProGlnGlnGluSerCysGlySerSerGlnLeuHis 44
Db 997 CTGACATACCTGTAAATCATGTGTCACAAAGGAAGATCATGTGATCCTCTCAGCTCCAT 1056
Qy 45 GluAsnSerGlySerProGlyIleThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64

Db 1057 GAAATAGTGGTCTCTCTGAAACTTCAAGTCCCTCCAGCTCCTCAAGACAATGATTTT 1116
Qy 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysCysProGlyAsnHis 84
Db 1117 TTATCTAGAAAAAGCTCAAGACTGTATTATTTATGAAGCTGCATCACTGTCTCGAAATCAC 1176
Qy 85 SerTyrAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
Db 1177 AGTTGGGATAGCACCAATTTCTGGATCTCAAGGGCTGCATTCTGTGATCAAGACCAATT 1236
Qy 105 ProCysSerSerAlaIleLeuAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
Db 1237 CCATGCTCTTACAGCAATAAATCCACTCTCACTGACGAGAACTCAGAACGCTCTGCAG 1296
Qy 125 ProGlyIleAlaGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
Db 1297 CCTGGTATAGCCAGCAGTGGATCCAGAGCAAAAGGAAGACATTGTGAACCAAAATGACA 1356
Qy 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164
Db 1357 GAAGCCTGCCTTAACCAAGTCGTAGATGCCCTTCTGTCCAGGACTTGTATCATGAAGAG 1416
Qy 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
Db 1417 GACTATGAACCTTGTATGATACCAAGCCTCAAGGACCTCAAAAGTCAGACAATTAAGAC 1476
Qy 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
Db 1477 ACTACTGACATCCAGAGGAAGATTTGCCAAGTTATAGTACAAAATTTGAAGATTAAC 1536
Qy 205 LysGlnMetGlyLeuGlnProTyrProGlyIleValSerArgSerProSerLeu 224
Db 1537 AAACAAATGGTCTTTCAGCCTTACCCGGAATACTTGTGTCTTAGATCACCATTCTTA 1596
Qy 225 AsnLeuLeuGlnAsnLysSerMet 232
Db 1597 AATTTACTTCAAAATAAAAGCATG 1620

RESULT 11

US-09-748-537-2
; Sequence 2, Application US/09748537
; Patent No: US20020061833A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Chao, Moses V.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-316001
; CURRENT APPLICATION NUMBER: US/09/748,537
; CURRENT FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US/09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US/09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-748-537-2

Alignment Scores:
Pred. No.: 5,39e-133 Length: 1931
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: 9 Gaps: 0

US-09-771-161a-93 (1-232) x US-09-748-537-2 (1-1931)

Qy 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24

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; LOCATION: (214) ... (1833)
US-09-728-721-1
Alignment Scores:
Pred. No.: 5,39e-133 Length: 1931
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: 9 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-728-721-1 (1-1931)
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24
DB 1150 AAGTTACAGAGGTTTCAAGTGCCCATTCACCTATGTGACAGAGAAATGGAATATCT 1209
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
DB 1210 CTGAACATACCTGTAAATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1269
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
DB 1270 GAAAAATAGTGGTTCTCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAAATGATTTT 1329
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
DB 1330 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGCTGGAAATCATC 1389
QY 85 SerTTPAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
DB 1390 AGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTCTGTGATCACAAGACCAT 1449
QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
DB 1450 CCATGCTCTTCAGCAATAATAAATCCACTCAACTGCAGGAACTCAGAACGCTCTGCAG 1509
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValGlnLysLeu 144
DB 1510 CTGGTATAGCCACAGAGTGGATCCAGAGCAAAAGGAGAGACATTTGTGACCAATGACA 1569
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuMetLysGlu 164
DB 1570 GAAGCCTGCCTTAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAAGAG 1629
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
DB 1630 GACTATGAACCTTGTAGTACCAAGGCTCAAGGACCTCAAAAGTCAGACAAATTTACTAGAC 1689
QY 185 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
DB 1690 ACTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAGATAAC 1749
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
DB 1750 AAAACAAATGGGTCTTCAGCCTTACCCGGAATACTTTGTGGTTTCTAGATCACCATCTTTA 1809
QY 225 AsnLeuLeuGlnAsnLysSerMet 232
DB 1810 AATTACTTCAAAATAAAAGCATG 1833

RESULT 13
US-10-133-780-2
; Sequence 1, Application US/09728721
; Patent No. US20020061845A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-124001
; CURRENT APPLICATION NUMBER: US/09/728,721
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/340,620
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
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; LOCATION: (214) ... (1833)
US-09-728-721-1
Alignment Scores:
Pred. No.: 5,39e-133 Length: 1931
Score: 1176.00 Matches: 226
Percent Similarity: 99.56% Conservative: 1
Best Local Similarity: 99.12% Mismatches: 1
Query Match: 97.51% Indels: 0
DB: 9 Gaps: 0

US-09-771-161A-93 (1-232) x US-09-728-721-1 (1-1931)
QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSer 24
DB 1150 AAGTTACAGAGGTTTCAAGTGCCCATTCACCTATGTGACAGAGAAATGGAATATCT 1209
QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
DB 1210 CTGAACATACCTGTAAATCATGGTCCACAGAGGAATCATGTGGATCCTCTCAGCTCCAT 1269
QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
DB 1270 GAAAAATAGTGGTTCTCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAAATGATTTT 1329
QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisCysProGlyAsnHis 84
DB 1330 TTATCTAGAAAAGCTCAAGACTGTTATTTATGAAGCTGCATCACTGCTGGAAATCATC 1389
QY 85 SerTTPAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
DB 1390 AGTTGGGATAGCACCATTTCTGGATCTCAAGGGCTGCATTCTGTGATCACAAGACCAT 1449
QY 105 ProCysSerSerAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
DB 1450 CCATGCTCTTCAGCAATAATAAATCCACTCAACTGCAGGAACTCAGAACGCTCTGCAG 1509
QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValGlnLysLeu 144
DB 1510 CTGGTATAGCCACAGAGTGGATCCAGAGCAAAAGGAGAGACATTTGTGACCAATGACA 1569
QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuMetLysGlu 164
DB 1570 GAAGCCTGCCTTAACAGTCGCTAGATGCCCTTCTGTCCAGGACTTGATCATGAAAGAG 1629
QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
DB 1630 GACTATGAACCTTGTAGTACCAAGGCTCAAGGACCTCAAAAGTCAGACAAATTTACTAGAC 1689
QY 185 ThrThrAspIleGlnGlyGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
DB 1690 ACTACTGACATCCAGGAGAGAAATTTGCCAAAGTTATAGTACAAAAATTTGAAGATAAC 1749
QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
DB 1750 AAAACAAATGGGTCTTCAGCCTTACCCGGAATACTTTGTGGTTTCTAGATCACCATCTTTA 1809
QY 225 AsnLeuLeuGlnAsnLysSerMet 232
DB 1810 AATTACTTCAAAATAAAAGCATG 1833

RESULT 13
US-10-133-780-2
; Sequence 2, Application US/10133780
; Publication No. US20020123115A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
; DOMAIN POLYPEPTIDES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
```

CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FastSeq for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/133,780
 FILING DATE: 26-Apr-2002
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/019,942
 FILING DATE: 06-FEB-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Meiklejohn, Ph.D., Anita L.
 REGISTRATION NUMBER: 35,283
 REFERENCE/DOCKET NUMBER: 07334/068001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1931 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-133-780-2

Alignment Scores:
 Pred. No.: 5,39e-133 Length: 1931
 Score: 1176.00 Matches: 226
 Percent Similarity: 99.56% Conservative: 1
 Best Local Similarity: 99.12% Mismatches: 1
 Query Match: 97.51% Indels: 0
 DB: 13 Gaps: 0

US-09-771-161A-93 (1-232) x US-10-133-780-2 (1-1931)
 QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
 Db 1150 AAGTTACAGAGTGTTCCTCAAGTCCATTACCTATGTGACAGAGAGAAATGGAATTATCT 1209
 QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
 Db 1210 CTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGGATCTCTCGAGCTCCAT 1269
 QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
 Db 1270 GAAATAGTGGTTCCTCAAGTCCCTCCAGGCTCTCTCAAGCAATGATTTT 1329
 QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84
 Db 1330 TTATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTCTCTGGAATCAC 1389
 QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
 Db 1390 AGTTGGGATAGACCATTTCTGGATCTCAAAAGGGTGCATTTCTGTGATCAAGACCAT 1449
 QY 105 ProCysSerSerAlaIleLeuAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
 Db 1450 CATGCTCTTCAGCAATTAATAATCACTCTCAACTGCAGGAAGTCTGAGACCAT 1509
 QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
 Db 1510 CTGTGTATAGCCAGCAGTGGATCAGAGCAAAAGGGAGACATTTGTGAACCAATGACA 1569
 QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164

Db 1570 GAAGCTGCTTAACACAGTGCCTAGATGCCCTTCTGTCCAGGGACTTGATCATGAAGAG 1624
 QY 165 AspTyrGluLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAsp 184
 Db 1630 GACTATGAACCTTTGTAGTACCAAGCCTTACCAAGGACCTCAAAAGTCAGACAAATTA 1689
 QY 185 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLysAspAsn 204
 Db 1690 ACTACTGCATCCCAAGGAGAGAAATTTGCCAAAGTTTATAGTACAAAAATTTGAAAGATA 1749
 QY 205 LysGlnMetGlyLeuGlnProTyrProGluIleLeuValValSerArgSerProSerLeu 224
 Db 1750 AAACAATGGTCTTCAGCCTTACCCGGAATACTTGTGTGTTTCTAGATCACCATCTTTA 1809
 QY 225 AsnLeuLeuGlnAsnLysSerMet 232
 Db 1810 AATTACTTCAAAAATAAAGCATG 1833

RESULT 14
 US-10-105-931-1
 ; Sequence 1, Application US/10105931
 ; Publication No. US20020150987A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bertin, John
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
 ; FILE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
 ; FILE REFERENCE: 07334-076001
 ; CURRENT APPLICATION NUMBER: US/10/105,931
 ; CURRENT FILING DATE: 2002-03-25
 ; PRIOR APPLICATION NUMBER: 09/099,041
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 09/019,942
 ; PRIOR FILING DATE: 1998-02-06
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1931
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (214)...(1833)
 US-10-105-931-1

Alignment Scores:
 Pred. No.: 5,39e-133 Length: 1931
 Score: 1176.00 Matches: 226
 Percent Similarity: 99.56% Conservative: 1
 Best Local Similarity: 99.12% Mismatches: 1
 Query Match: 97.51% Indels: 0
 DB: 13 Gaps: 0

US-09-771-161A-93 (1-232) x US-10-105-931-1 (1-1931)
 QY 5 GlnLeuGlnSerValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSer 24
 Db 1150 AAGTTACAGAGTGTTCCTCAAGTCCATTACCTATGTGACAGAGAGAAATGGAATTATCT 1209
 QY 25 LeuAsnIleProValAsnHisGlyProGlnGluSerCysGlySerSerGlnLeuHis 44
 Db 1210 CTGAACATACCTGTAATCATGTGTCACAGAGGAATCATGTGGATCTCTCGAGCTCCAT 1269
 QY 45 GluAsnSerGlySerProGluThrSerArgSerLeuProAlaProGlnAspAsnAspPhe 64
 Db 1270 GAAATAGTGGTTCCTCAAGTCCCTCCAGGCTCTCTCAAGCAATGATTTT 1329
 QY 65 LeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHis 84
 Db 1330 TTATCTAGAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTCTCTGGAATCAC 1389
 QY 85 SerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysThr 104
 Db 1390 AGTTGGGATAGACCATTTCTGGATCTCAAAAGGGTGCATTTCTGTGATCAAGACCAT 1449
 QY 105 ProCysSerSerAlaIleLeuAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 124
 Db 1450 CATGCTCTTCAGCAATTAATAATCACTCTCAACTGCAGGAAGTCTGAGACCAT 1509
 QY 125 ProGlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMetThr 144
 Db 1510 CTGTGTATAGCCAGCAGTGGATCAGAGCAAAAGGGAGACATTTGTGAACCAATGACA 1569
 QY 145 GluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGlu 164

